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(UYLE-) RIJKSUNIV LEIDEN
         02-JUN-1998;
23-JUL-1997;
                        23-JUL-1998;
                                  04-FEB-1999
                                           WO9905313-A2
                                                             Intron; minor histocompatibility antigen HA-1; typing allele; H allele; R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant; severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
                                                                                       HA-1 R-allele
                                                                                                 13-MAY-1999
                                                                                                                    AAW97374 standard; Protein;
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97EP-0202303.
                        98WO-EP04928
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RESULT 2
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Best Local
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The present sequence represents part of the minor histocompatibility antigen HA-1 H-allele. The specification describes methods for typing
                                              Claim 18; Fig 5; 59pp; English.
                                                                                 detection
                                                                                       Typing minor histocompatibility antigen HA-1 - by amplifying and identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g.
                                                                                                                                        WPI; 1999-142960/12.
                                                                                                                                                                                                                               02-JUN-1998;
23-JUL-1997;
                                                                                                                                                                                                                                                                                                         04-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents part of the minor histocompatibility antigen HA-1 R-allele. The specification describes methods for typing alleles (preferably the H and R alleles) of the minor histocompatibility antigen HA-1 in a sample, which comprise detecting polymorphic nucleotides in the cDNA or genomic nucleic acids of the alleles. The methods can be used for HA-1 typing for bone marrow transplants, severe aplastic anaemia, leukaemia and immune deficiency diseases, as well as detection of genetic aberrances. The probes and primers of the invention can be used to screen for the HA-1 alleles. The HA-1 peptides can be used anti-idiotypic B cells and/or T cells and antibodies.
                                                                                                                                                                                                   (UYLE-) RIJKSUNIV LEIDEN
                                                                                                                                                                                                                                                                           23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                       W09905313-A2
                                                                                                                                                                                                                                                                                                                                                                                              Intron; minor histocompatibility antigen HA-1; typing allele; H allele; R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant; severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAY-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Fig 5; 59pp; English.
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                                                                              of genetic aberrances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA;
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97EP-0202303
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88.9%;
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Pred. No. 7.8e+05;
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RESULT 3
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-cell epitope from the minor histocompatibility antigen HA-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW97572 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neoplastic haematopoietic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-cell epitope; minor histocompatibility antigen HA-1; vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                        The present sequence represents an immunogenic peptide constituting a T-cell epitope, obtainable from the minor histocompatibility antigen HA-1. The peptide can be used in vaccines or pharmaceutical formulations as medicines to induce tolerance for transplants so as to prevent rejection and/or Graft-versus-Host Disease, or to treat autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                         23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9905173-A1
                                                                                                                                                                                                                                                                               WPI; 1999-142855/12.
                                                                                                                                                                                                                                                                                                             Engelhard VH,
                                                                                                                                                                                                                                                                                                                                           (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                            23-JUL-1997;
                                               diseases. Neoplastic haematopoietic cells presenting the peptides, in an HLA class I context, can be eliminated after specific recognition of the peptides. The peptides can also be used to raise antibodies,
                                                                                                                                                                                     Claim 1; Page 39; 57pp; English.
                                                                                                                                                                                                                 or graft-versus-host disease
                                                                                                                                                                                                                                 Immunogenic peptide from minor histocompatibility antigen HA-1 useful for inducing tolerance to transplants and prevent rejection
Sequence
                             of the peptides. The peptides ca
T-cell receptor, B- and T-cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rejection; Graft-versus-Host Disease; autoimmune disease;
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   9 AA;
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                                                                                                                                                                                                                                                                                                               Goulmy EAJM,
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Pred. No. 7.8e+05;
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Query Match

Score 36;

DB 20;

Length 9;

RESULT 5

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AAW99196 standard; peptide;

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Matches 9; Conservative (
                                                               Query Match
Best Local
                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minor histocompatibility antigen HA-1 T-cell epitope #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; aplastic anaemia; immune deficiency disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minor histocompatibility antigen; HA-1; T-cell epitope; immunological; graft versus host disease; bone marrow transplant; leukaemia; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                      The present sequence represents a new peptide (P1) constituting a T-cell epitope obtainable from the minor histocompatibility antigen HA-1. The peptide is immunogenic and can be used as part of a vaccine. P1 is used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the
                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                      A new minor histocompatibility antigen, HA-1 - useful to treat
                                                                                                                                                                                                                                                                                                                                                             Engelhard VH,
                                                                                                                                                                                                                                                                                                                                                                                     (UYLE-) RIJKSUNIV LEIDEN
                                                                                                                                                                                                                                                   Claim 1; Page 32; 47pp; English.
                                                                                                                                                                                                                                                                             immune diseases and prevent rejection and host versus graft disease in bone marrow and organ transplantation
                                                                                                                                                                                                                                                                                                                                     WPI; 1999-153312/13.
                                                                                                       Sequence
                                                                                                                                diseases
                                                                                                                                            treatment of severe aplastic anaemia, leukaemia, and immune deficiency
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                                                                 Local Similarity
1 VLXDDLLEA 9
                         1 VLXDDLLEA 9
                                                  9;
                                                                                                        9 AA;
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                             Goulmy EAJM, Hunt DF;
                                                                                                                                                                                                                                                                                                                                                                                                                   97EP-0202303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= His, Arg
                                                                 94.7%; Score 36; 100.0%; Pred. No.
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0; Mismatches 0;
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). 7.8e+05;
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AAW99197
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 23-JUL-1998;
                                                                                              diagnosis; aplastic anaemia; immune deficiency disease.
                                                                                                         Minor histocompatibility antigen; HA-1; T-cell epitope; immunological; graft versus host disease; bone marrow transplant; leukaemia; vaccine;
                                                    W09905174-A1
                                                                             Homo sapiens
                                                                                                                                                Minor histocompatibility antigen HA-1 T-cell epitope #3.
                                                                                                                                                                                20-MAY-1999 (first entry)
                                                                                                                                                                                                               AAW99197;
                                                                                                                                                                                                                                 AAW99197 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                     and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the treatment of severe aplastic anaemia, leukaemia, and immune deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 32; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A new minor histocompatibility antigen, HA-1 - useful to treat immune diseases and prevent rejection and host versus graft disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-153312/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in bone marrow and organ transplantation
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                                                                                                                                                                                                                                                                                                                            1 VLXDDLLEA 9
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                                                                                                                                                                                                                                                                                                                                                     Conservative
98WO-NL00425
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The present invention describes a new peptide (P1) constituting a T-cell
                                  Disclosure; Page 31; 47pp; English.
                                                                       A new minor histocompatibility antigen, HA-1 - useful to treat immune diseases and prevent rejection and host versus graft di
                                                            in bone marrow and organ transplantation
                                                                                                                         N-PSDB; AAX19408.
                                                                                                                                                                  Engelhard VH,
                                                                                                                                                                                            (UYLE-) RIJKSUNIV LEIDEN
                                                                                                                                                                                                                         23-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                    Minor histocompatibility antigen; HA-1; T-cell epitope; immunological; graft versus host disease; bone marrow transplant; leukaemia; vaccine; diagnosis; aplastic anaemia; immune deficiency disease.
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                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a new peptide (PI) constituting a T-cell epitope obtainable from the minor histocompatibility antigen HA-1. The peptide is immunogenic and can be used as part of a vaccine. PI is used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the treatment of severe aplastic anaemia, leukaemia, and immune deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                  DH cell KIAA0223 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                20~MAY-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW99198 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 15; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in bone marrow and organ transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-153312/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Engelhard VH, Goulmy EAJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYLE-) RIJKSUNIV LEIDEN.
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                                                                                                                                       1999-153312/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                               Goulmy EAJM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.7%;
88.9%;
                                                                                                                                                             Hunt DF;
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Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                       disease
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RESULT 8
AAW99199
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                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epitope obtainable from the minor histocompatibility antigen HA-1. The peptide is immunogenic and can be used as part of a vaccine. Plis used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the treatment of severe aplastic anaemia, leukaemia, and immune deficiency diseases. The present sequence represents a KIAA0223 sequence given in the present invention.
 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minor histocompatibility antigen; HA-1; T-cell epitope; immunological; graft versus host disease; bone marrow transplant; leukaemia; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW99199 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; aplastic anaemia; immune deficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vR cell KIAA0223 protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW99199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                                                               The present invention describes a new peptide (P1) constituting a T-cell epitope obtainable from the minor histocompatibility antiqen HA·1. The peptide is immunogenic and can be used as part of a vaccine. P1 is used as a medicine, to induce tolerance for transplants, prevent rejection and/or graft versus host disease, or to treat (auto) immune diseases. In particular it can be used with bone marrow transplantation, in the
                                                                                                                                                                                                                                                                  A new minor histocompatibility antigen, HA-1 - useful to treat immune diseases and prevent rejection and host versus graft disease in bone marrow and organ transplantation \,
                                                                                                                                                                                                                                                                                                                                                                           Engelhard VH,
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                                                                                                                                                                                                                                                                                                                                                                                                        (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                         Disclosure; Page 31; 47pp; English.
                                                        Sequence
                                                                                                  treatment of severe aplastic anaemia, leukaemia, and immune deficiendiseases. The present sequence represents a KIAA0223 sequence given
                                                                                      in the present invention.
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Local Similarity
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                                                           13 AA;
Conservative
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                 94.7%;
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Pred. No. 0.69;
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                Score 36; DB 2
Pred. No. 0.69;
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    Mismatches
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      1; Indels
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RESULT 9
AAW97414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIAA0223 polymorphism in HA-1 negative homozygous individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW97414;
                                                                                                                                                                                                                                                                                                                                    The present sequence represents the KIAA0223 polymorphism in HA-1 negative homozygous individuals. The specification describes an immunogenic peptide constituting a T-cell epitope, obtainable from the minor histocompatibility antigen HA-1. The peptide can be used in vaccines or pharmaceutical formulations as medicines to induce tolerance for transplants so as to prevent rejection and/or craft-versus-Host Disease, or to treat autoimmune diseases. Neoplastic graft-versus-Host Disease, or to treat autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 38; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX16080.
                                                                                                                                                                                                                                                                                           haematopoietic cells presenting the peptides, in an HLA class I context, can be eliminated after specific recognition of the peptides. The peptides can also be used to raise antibodies, T-cell receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic peptide from minor histocompatibility antigen HA-1 - useful for inducing tolerance to transplants and prevent rejection
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                                                                                                                                                                                                                                                   Sequence
               20-MAY-1999
                                                                  AAW97415 standard; Protein; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VLHDDLLEA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VLXDDLLEA 9
                                                                                                                                                                                                             Local
                                                                                                                                        3 VLRDDLLEA 11
                                                                                                                                                                                                                                                                                  and T-cells.
                                                                                                                                                                   1 VLXDDLLEA 9
                                                                                                                                                                                              al Similarity
8; Conserv
                                                                                                                                                                                                                                                        3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                 Conservative
               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goulmy EAJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97EP-0202303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-NL00424
                                                                                                                                                                                                                  94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hunt DF;
                                                                                                                                                                                                   0;
                                                                                                                                                                                                                  Score 36; DB 2
Pred. No. 0.69;
                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                DB 20; Length 13;
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В
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                                                                                                                                                                                                                                                                        RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
 20-NOV-1998;
                                                      W09927105-A2
                                                                             Chlamydia pneumoniae.
                                                                                                     vaccine; neutralising epitope.
                                                                                                                      sinusitis;
                                                                                                                         Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
                                                                                                                                                    Chlamydia pneumoniae transmembrane protein sequence.
                                                                                                                                                                                    13-SEP-1999 (first entry)
                                                                                                                                                                                                                    AAY34986;
                                                                                                                                                                                                                                       AAY34986 standard; Protein; 192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      positive homozygous individuals. The specification describes an immunogenic peptide constituting a T-cell epitope, obtainable from the minor histocompatibility antigen HA-1. The peptide can be used in vaccines or pharmaceutical formulations as medicines to induce tolerance for transplants so as to prevent rejection and/or Graft-versus-Host Disease, or to treat autoimmune diseases. Neoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                haematopoietic cells presenting the peptides, in an HLA class I can be eliminated after specific recognition of the peptides. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptides can also be used to raise antibodies, T-cell receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the KIAA0223 polymorphism in HA-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 38; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic peptide from minor histocompatibility antigen HA-1 -useful for inducing tolerance to transplants and prevent rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Engelhard VH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-cell epitope; minor histocompatibility antigen HA-1; vaccine; transplant rejection; Graft-versus-Host Disease; autoimmune disneoplastic haematopoietic cell; KIAA0223 polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX16081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIAA0223 polymorphism in HA-1 positive homozygous individuals
                                                                                                                                                                                                                                                                                                             3 VLHDDLLEA 11
                                                                                                                                                                                                                                                                                                                                       1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                and T-cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999-142855/12.
                                                                                                            purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                       13 AA;
                                                                                                                                                                                                                                                                                                                                                                Conservative
98WO-IB01890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goulmy EAJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97EP-0202303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-NL00424
                                                                                                                                                                                                                                                                                                                                                                          94.7%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 2
Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hunt DF;
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    DB 20; Length 13;
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                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             context,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Propionibacterium acnes polypeptides and nucleic acids useful for
                                          N-PSDB; AAS59559
                                                                                                                                                          02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
                                                                                  L'maisonneuve J,
                                                                                                     Skeiky YAW,
                                                                                                                                                                           21-APR-2000; 2000US-199047P. 02-JUN-2000; 2000US-208841P.
                                                                                                                                                                                                                  20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                   01-NOV-2001
                                                                                                                                                                                                                                                                                                                                       SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                              (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                              WO200181581-A2.
                                                                                                                                                                                                                                                                                                           Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                              dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes immunogenic protein #14122
                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU53226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU53226 standard; Protein; 226 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease, sarcoidosis, Sinusitis, purulent offits media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see ANY34584-Y35879) can be used in nucleotides sequences can also be used as immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 896; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-357842/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 VLAEDLLEA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VLXDDLLEA 9
                                                        2001-616774/71
                                                                                                Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0107078.
97FR-0014673.
                                                                                  Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.8%;
77.8%;
                                                                              Mitcham JL, Wang, Jen S, Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB
Pred. No. 47;
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                                                                                          Wang SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Length 192;
                                                                                          Bhatia A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides. The proteins and their associated DNA sequences are use
the treatment, prevention and diagnosis of medical conditions caused
P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccinating against and diagnosing infections, especially useful for treating acne vulgaris \mbox{\ \ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAU39105-AAU68017 represent Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID No 14421; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                Chlamydial infection; antigen; immunogen; vaccine; diagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carotid artery stenosis; myocardial infarction; cerebrovascular disease; aortic aneurysm; claudication; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB90575 standard; Protein; 499 AA
                                                                                                                                                                                                                                                                                                                                                                 strain CWL029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae cp6664 protein, SEQ ID NO:99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-2002 (first entry)
                                                                                                                                                                                                                                                            10-JAN-2002
                                                                                                                                                                                                                                                                                               WO200202606-A2
                                                                                                                                                                                                                                                                                                                                Chlamydia pneumoniae
                                                                                                                                         21-JUL-2000;
07-AUG-2000;
                                                                                                                                                                                         03-JUL-2000;
                                                                                                                                                                                                                           03-JUL-2001;
                                                                                                                       18-AUG-2000;
                                                                                                                                                                        11-JUL-2000;
                                  (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                    2000GB-0016363.
2000GB-0017047.
2000GB-0017983.
2000GB-0019368.
2000GB-002583.
2000GB-002583.
2000GB-002583.
                                                                                                                                                                                                                           2001WO-IB01445.
                                                                     2000GB-0031706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogenic
are used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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AAY92707
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Best Local Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                  myocardial infarction, cerebrovascular disease, aortic aneurysm, claudication and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched DNA probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a specifically claimed Chlamydia pneumoniae protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as atherosclerosis, coronary artery disease, carotid artery stenosis, atherosclerosis, coronary artery disease, carotid artery stenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 89-90; 364pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         PKS; type I; 8,8a-deoxyoleandolide synthase; modular; ketosynthase; acyl-transferase; acyl-carrier protein; inactivated; polyketide; macrolactone; antibiotic; motilide; erythromycin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oleandomycin; oleandolide; polyketide synthase; oleAI; oleAII; oleAIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s. antibioticus 8,8a-deoxyoleandolide synthase I encoded by oleAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY92707 standard; Protein; 4150 AA.
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                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
Domain
                                                         Domain
                                                                                            Region
                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395 VLAEDLLEA 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                        antibioticus
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                       /label=
                                                                                                                                                                        /note= "malonyl-specific acyl transferase domain"
                                                                                                                                                                                                 /label= AT_domain
                                                                                                                                                                                                                                    /note= "inactivated ketosynthase domain"
                                                                                                                                                                                                                                                         /label= KS-Q_domain
                                                                                                                                                                                                                                                                                            /label= Loading_module
    1580..1926
                                         /label=
                                                                                /label=
                                                                                                                 note= "acyl
                    'note= "ketosynthase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.8%;
77.8%;
                                                       :1= Extender_module_1
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                                         KS1_domain
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Pred. No. 1.
                                                                                                                                         _domain
                                                                                                                     carrier protein domain"
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1.3e+02;
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N-PSDB; AAA09469
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                                                                                                                                                                                                                  (KOSA-) KOSAN BIOSCIENCES INC
                                                                                                                                                                                                                              16-FEB-1999;
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                                                                                                                                                                                                                                              22-OCT-1999;
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                                                                                                                                                                                                                             98US-0106100.
99US-0120254.
                                                                                                                                                                                                                                             99WO-US24478
                                                                                                                                                                                                                                                                           'note= "acyl carrier protein domain"
                                                                                                                                                                                                                                                                                  /label= ACP2_domain
                                                                                                                                                                                                                                                                                            /note= "ketoreductase domain'
                                                                                                                                                                                                                                                                                                 /label= KR2_domain
                                                                                                                                                                                                                                                                                                                   /label= AT2_domain
                                                                                                                                                                                                                                                                                                                                                                     /note= "ketoreductase domain"
                                                                                                                                                                                                                                                                                                                              'note≖
                                                                                                                                                                                                                                                                                                                                                           /label= ACP1_domain
                                                                                                                                                                                                                                                                                                                                                                                            /label= AT1_domain
                                                                                                                                                                                                                                                                                        .4075
                                                                                                                                                                                                                                                                                                        .388
                                                                                                                                                                                                                                                                                                                        .3420
                                                                                                                                                                                                                                                                                                                                                                                  . 2349
                                                                                                                                                                                                                                                                                                                                       . 297
                                                                                                                                                                                                                                                                                                                                                  . 4069
                                                                                                                                                                                                        McDaniel R,
                                                                                                                                                                                                                                                                                                           "acyl transferase domain"
                                                                                                                                                                                                                                                                                                                           "ketosynthase domain"
                                                                                                                                                                                                                                                                                                                                                      "acyl carrier
                                                                                                                                                                                                                                                                                                                                                                                     "acyl transferase domain"
                                                                                                                                                                                                                                                                                                                                                                            KR1_domain
                                                                                                                                                                                                                                                                                                                                  KS2_domain
                                                                                                                                                                                                                                                                                                                                           Extender_module_2
                                                                                                                                                                                                       Tang L;
                                                                                                                                                                                                                                                                                                                                                      protein domain"
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Recombinant DNA compound encoding oleandolide polyketide synthase for synthesizing polyketides comprising a coding sequence for a domain of a loading module or any one of extender modules

Disclosure; Page 27-28; 86pp; English.

module 1 KS domain is inactivated by deletion or other mutation. In particular, the inactivation is mediated by a change in the KS domain that renders it incapable of binding substrate (the KSI-o mutation), rendered by mutation in the codon for the active site cysteine. The oleandolide PKS is useful for synthesizing polyketides, which are useful as antibiotics and motilides. Heterologous expression of oleandolide PKS in host cells such as Streptomyces coelicolor and S. lividans is also made possible. Unmodified oleandolide compounds can be provided to coding sequence for a domain of loading module or any one of extender modules 1-4 or 1-6, including an oleandolide PKS operably linked to a promoter. Also discussed are recombinant oleandolide PKS in which the contains an inactivated KS, called KS-0, where Q is the abbreviation for glutamine, present instead of the active site cysteine required for activity. The large multifunctional PKS enzymes catalyze the biosynthesis of polyketide macrolactones through multistep pathways involving decarboxylative condensations between acylthioseters followed by cycles the first ORF also encodes the loading module. Each module is composed of at least a ketosynthase (KS), acyl-transferase (AT) and an acyl carrier protein (ACP) domain. The oleandolide PKS loading module contains an inactivated KS, called KS-Q, where Q is the abbreviation for The oleandolide polyketide synthase (PKS), also known as 8.8a-deoxyoleandolide synthase, is encoded by three open reading frames (ORF), designated oleAI, oleAII and oleAIII. The PKS is a type I "modular" enzyme, where each ORF encodes 2 extender modules and glycosylation to yield oleandomycin, glycosylation to yield oleandomycin, an antibacterial polyketide. The invention concerns an isolated recombinant DNA compound, comprising a varying beta-carbon processing activities. The macrolide product of PKS, 8,8a-deoxyoleandolide, is further modified by epoxidation and ycosylation to yield oleandomycin, an antibacterial polyketide. The of Saccharopolyspora erythraea and converted to the

Query Match Best Local Similarity

81.6%;

Score 31; Pred. No.

DB

21;

Length 149;

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PF
PR
PR
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
AAB25210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                        senescence of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life
                                                                                                                         signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced a altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance
 Sequence
                      between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot-free clear wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                      pine (Pinus radiata also known as Monterey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external
                                                                                                                                                                                                                                                                                        AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 235; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         to external signals
                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strabala TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-476052/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2000; 2000WO-US00724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eucalyptus grandis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elongation; survival; disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eucalyptus grandis; Pinus radiata; Monterey pine; plant; plant cell signalling; modulation; transgenic plant; pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200042171-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     environmental change;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1781 LRDDLLEA 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eucalyptus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB25210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB25210 standard; Protein; 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              corresponding derivatives of erythromycins A-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               grandis cell signalling involved protein SEQ ID NO:529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .Nieuwenhuizen NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0228986
99US-0162866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.2%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulation; transgenic plant; pathogen; growth; development; cell proliferation; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.9e
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nutrient metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modification;
thogen; growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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B οy

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RESULT 16
ABB48245
                                                                                                                                                                                                                                                                                                     The present invention relates to the genome sequence of Listeria CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. CC monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein cencoded by the genome sequence of the present invention. Proteins cantibodies, identification of L. monocytogenes and related organisms, and cfor biosynthesis and biodegradation, especially biosynthesis of Vitamin CC selecting compounds that regulate gene expression and cell replication CC selecting compounds that regulate gene expression and cell replication CC and modulate L. monocytogenes related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and compounds that regulate gene expression and cell replication can decines compositions for the treatment or prevention of infections by L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Denous L, Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Denous L, Goesart Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, 'Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Daniels J, Gerrido-García P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Baquero F, García Del Portillo F, Gomez-Lopez N; Chakraborty T, Chakrabo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200177335-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2000; 2000FR-0004629
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                                                                                                                                                                                                                     monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; SEQ ID No 950; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-010914/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2001; 2001WO-FR01118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related polypeptides
                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 ILLDELLEA 81
Local Similarity
nes 6; Conser
                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLXDDLLEA 9
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                                                                                                                              276 AA;
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                              81.6%;
75.0%;
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                                 Score 31; DB 23; Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1:
                                                            Length 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Matches

Conservative

1;

Mismatches

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Gaps

12-MAR-2002 AAU73000;

(first entry)

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                           RESULT 18
                                                                                                                                            Matches
                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                    The invention relates to a peptide (I) encoded by an operon (II) of Neisseria meningitidis including virulence genes, or a related molecule having a 40% sequence similarity at the peptide or nucleotide level in a Gram-negative bacterium, or its functional fragment, for therapeutic or diagnostic use. (I) and (II) are useful in the manufacture of a medicament for treating or preventing a condition (e.g., meningitis) associated with infection by Neisseria or Gram-negative bacteria. The product is useful for veterinary treatment and in a screening assay for the identification of an antimicrobial drug. The vaccines have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU72987 standard; Protein; 289 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide encoded by operon including virulence genes of Neisseria meningitidis, useful as vaccine component for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2001; 2001WO-GB02003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis virulence protein #77.
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 319-320; 423pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         meningitis and for identifying antimicrobial drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-066593/09.
N-PSDB; AAS97272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-2000; 2000GB-0011108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meningitis; virulence; gene; antibacterial; vaccine; veterinary;
AAU73000 standard; Protein;
                                                                                                                                                                                                                                            virulence proteins of the invention.
                                                                                                                                                                                                                                                          prophylactic applications. AAU72911-AAU73014 represent N. meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROSCIENCE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection; Gram-negative bacteria; antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 ISDDLLEA 172
                                                                              130 ILADDLIDA 138
                                                                                                                                            Local Similarity hes 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LXDDLLEA 9
                                                                                                           1 VLXDDLLEA 9
                                                                                                                                                                                                           289 AA;
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                             81.6%;
                                                                                                                                                             Score 31; DB 23;
Pred. No. 1.8e+02;
                                                                                                                                               Mismatches
                                                                                                                                                                              Length 289;
                                                                                                                                               0,
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Neisseria meningitidis virulence protein #90

18

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RESULT 19
ABB59345
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
---hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                      Qy
23-MAR-2000; 2000US-191637P
                         23-MAR-2001; 2001WO-US09231
                                                                                                          Drosophila melanogaster
                                                                               WO200171042-A2
                                                                                                                                   pharmaceutical.
                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 4827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostic use. (I) and (II) are useful in the manufacture of a medicament for treating or preventing a condition (e.g., meningitis) associated with infection by Neisseria or Gram-negative bacteria. The product is useful for veterinary treatment and in a screening assay for the identification of an antimicrobial drug. The vaccines have prophylactic applications. AAU72911-AAU73014 represent N. meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a peptide (I) encoded by an operon (II) of Neisseria meningitidis including virulence genes, or a related molecule having a 40% sequence similarity at the peptide or nucleotide level in a Gram-negative bacterium, or its functional fragment, for therapeutic or
                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                          ABB59345 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 366-367; 423pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide encoded by operon including virulence genes of Neisseria meningitidis, useful as vaccine component for treating or preventing meningitis and for identifying antimicrobial drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                              virulence proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-066593/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS97285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-2000; 2000GB-0011108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-2001; 2001WO-GB02003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-NOV-2001
                                                                                                                                                                                                                                                                                                                            130 ILADDLIDA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MICR-) MICROSCIENCE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200185772-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection; Gram-negative
                                                                                                                                                                                                                                                                                                                                                       1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                   289 AA;
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virulence;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                          Protein; 1042
                                                                                                                                                                                                                                                                                                                                                                                            81.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene; antibacterial; vaccine; veterinary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacteria; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                               ω
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                                                                                                                                                                                                                                                                                                                                                                                            Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Length 289;
                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 20
AAU86478
ID AAU86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
"~+~hes 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                              18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB01847-ABB72072).
                                                                                                                      16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                               17-JAN-2001;
                                                                                                                                                                                                                                         02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                          Novel human connective tissue related polypeptide #44.
                                                                                                                                                                                                                                                                                                                                                                      21-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  AAU86478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                   Human; connective tissue related disorder; cancer; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                          AAU86478 standard; Protein; 94 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 4827; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABL03448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          595 VLFDDALEA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VLXDDLLEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1042 AA;
2000US-0215135.

2000US-0216647.

2000US-0216880.

2000US-0217487.

2000US-0217496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M,
                                                                2000US-0209467.
2000US-0214886.
                                                                                          2000US-0205515
                                                                                                         2000US-0198123
                                                                                                                    2000US-0190076
                                                                                                                                  2000US-0189874
                                                                                                                                                2000US-0186350
                                                                                                                                                             2000US-0184664
                                                                                                                                                                          2000US-0180628
                                                                                                                                                                                                               2001WO-US01322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.6%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB 22
Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers EW
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14-JUL-2000; 26-JUL-2000;

2000US-0218290. 2000US-0220963. 2000US-0220964. 2000US-0224518. 2000US-0224519. 2000US-0225213. 2000US-0225214. 2000US-0225266. 2000US-0225266.

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08-NOV-2000;
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17-NOV-2000)
17-NOV-2000)
17-NOV-2000)
17-NOV-2000)
17-NOV-2000)
17-NOV-2000)
01-DEC-2000)
05-DEC-2000)
05-DEC-2000)
05-DEC-2000)
06-DEC-2000)
06-DEC-2000)
08-DEC-2000)
08-DEC-2000]
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
The present invention relates to the isolation of novel human connective tissue related polypeptides and the polynucleotide (cDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. AAU86435-AAU86923 represent the novel human connective tissue related polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                          Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis -
                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                   N-PSDB; ABK41656.
                                                                                                                                                                                                                                                                                          Rosen CA,
                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                               2001-565190/63.
                                                                                                                                                                   11;
                                                                                                                                                                   SEQ ID No 543; 673pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US - 0246474.
2000US - 0246475.
2000US - 0246476.
2000US - 0246477.
2000US - 0246524.
2000US - 0246524.
2000US - 0246525.
2000US - 0246526.
2000US - 0246527.
2000US - 0246528.
2000US - 0246528.
2000US - 0246610.
2000US - 0246611.
2000US - 0246613.
2000US - 0246613.
2000US - 0249207.
2000US - 0249207.
2000US - 0249210.
2000US - 0249210.
2000US - 0249211.
2000US - 0249211.
                                                                                                                                                                                                                                                                                          Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0249213
2000US-0249214
2000US-0249215
2000US-0249216
2000US-0249217
2000US-0249218
2000US-0249218
2000US-0249244
2000US-0249245
2000US-0249245
2000US-0249264
2000US-0249265
2000US-0249267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0249299.
2000US-0249300.
2000US-0250160.
                                                                                                                                                                                                                                                                                                                                             2000US-0251989.
2000US-0251990.
2000US-0254097.
2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0251856.
2000US-0251868.
2000US-0251869.
                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0250391
                                                                                                                                                                                                                                                                                                                       SCI INC
                                                                                                                                                                                                                                                                                          Ruben SM;
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14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-022568.
2000US-0225447.
2000US-0225479.
2000US-0225758.
2000US-0225759.
2000US-0225759.
2000US-0226681.
2000US-0226868.
2000US-0226868.
2000US-0228824.
2000US-0228824.
2000US-0229343.
2000US-0229343.
2000US-0239345.
2000US-0239345.
2000US-0231243.
2000US-0231249.
2000US-0232401.
2000US-0233063.
2000US-0233484.
2000US-0233484.
2000US-0233484.
2000US-02334836.
2000US-0233498.
2000US-0233498.
2000US-0233498.
2000US-0233680.
2000US-0235836.
2000US-0235836.
2000US-0235836.
2000US-0235836.
2000US-0235836.
2000US-0235836.
2000US-0235836.
2000US-023680.
2

14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
21-OCT-2000;
02-OCT-2000;
01-NOV-2000;

14-AUG-2000)
12-AUG-2000)
22-AUG-2000)
22-AUG-2000)
23-AUG-2000)
23-AUG-2000)
21-SEP-2000)
01-SEP-2000)
01-SEP-2000]

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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon CC cancer-associated nucleic acid molecules (N) and proteins (P), where CC the proteins are collectively known as colon cancer antigens. The colon CC cancer antigens have cytostatic activity and can be used in gene CC diagnosis and treatment of diseases associated with inappropriate P CC expression. For example, N and P may be used in the prevention, CC associated with decreased expression by rectifying mutations or deletions CC in a patient's genome that affect the activity of P by expressing CC inactive proteins or to supplement the patients own production of P. CC distributions of the nucleic acids into a host cell and culturing the cell CC to express the proteins. N and P can be used in the prevention, diagnosis CC and AAB377789 represent sequences used in the examplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
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       Matches
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                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                   present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 6423-6425; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAH33292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200122920-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colorectal carcinoma; chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human colon cancer antigen protein SEQ ID NO:4625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-SEP-2001 (first entry)
       Local Similarity hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG73861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG73861 standard; Protein; 328 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 LSDDLLES 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                              328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barash SC,
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0157137.
99US-0163280.
                  78.98;
75.0%;
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75.0%;
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    1;
                Score 30; DB 22;
Pred. No. 3.3e+02;
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Pred. No.
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 94;
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                            Length 328;
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 0;
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Gaps
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0,
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XX DXX
                                                                                                                                 RESULT 23
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AAB96742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PN XX
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                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                       Best
Sorangium cellulosum non-ribosomal peptide synthetase EPOS p.
                                       10-APR-2000
                                                                       AAY58574;
                                                                                            AAY58574 standard; Protein; 1410 AA
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial
                                                                                                                                                                                                                                                                                                                                  uses, since the proteins are stable at very high temperatures, some uses centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143,
                                                                                                                                                                          472 IVEDDLIEA 480
                                                                                                                                                                                                                                                                                                                          AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Pages 1507-1509; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleotide sequences isolated from Pyrococcus abyssi encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Forterre P,
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins useful in industry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-126236/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative P. abyssi type I site specific endonuclease, subunit M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FR2792651-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB96742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB96742 standard; Protein; 623 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-OCT-2001 (first entry)
                                                                                                                                                                                                                                     les 5; Conser
                                                                                                                                                                                                       1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 VLKDDILE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VLXDDLLE 8
                                                                                                                                                                                                                                                                                               623 AA;
                                                                                                                                                                                                                                    Conservative
                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thierry JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weissenbach J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99FR-0005034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99FR-0005034.
                                                                                                                                                                                                                                                  78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prieur D,
                                                                                                                                                                                                                                    ω
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                                                                                                                                                                                                                                             Score 30; DB 22;
Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saurin W,
                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dietrich J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heilig R;
                                                                                                                                                                                                                                                            Length 623;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                               some up to
                                                                                                                                                                                                                            0,
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CC starter unit; polyketides being synthesised from two-carbon building CC blocks, the beta-carbon of which always carries a keto group. Each round CC blocks, the beta-carbon of which always carries a keto group. Each round CC of two-carbon addition is carried out by a complex of enzymes known as CC the polyketide synthase in a manner similar to fatty acid biosynthesis. CC the polyketide synthase in a manner similar to fatty acid biosynthesis. CC carbon A (AAY58573) and EPOS P (AAY58574) are involved in formation of CC the thiazole ring formation of epothilones, and EPOS B, EPOS C, EPOS D CC and EPOS E (AAY58575-Y58578) are involved in polyketide backbone CC depothilones orf 3 (AAY58579) is an epothilone macrolactone oxidase, and CC compositions orf 3 (AAY58582) and Orf14 (AAY38593) are thought to be compositions. Epothilones exhibit a much lower drop in potency against a compositions. Epothilones exhibit a much lower drop in potency against a compositions. Epothilones exhibit a much lower drop in potency against a composition of epothilones are too compared with taxol, and are untility drug-resistant cell line compared with taxol, and are considerably less efficiently exported from such cells by the multidrug considerably less efficiently exported from such cells by the multidrug considerably less efficiently exported from such cells by the multidrug synthesis, and Sorangium cellulosum is difficult to ferment, produce on a geothilones are too complex for industrial scale chemical synthesis, and Sorangium cellulosum is difficult to ferment, producing consider for the recombinant production of epothilones in a heterologous host
                                                                         RESULT 24
AAU02010
ID AAU07
                                                                                                                                                                                                                     Ş
                                                                                                                                                                                g
  DX AX
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9966028-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorangium cellulosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPOS P; non-ribosomal peptide synthetase; polyketide synthase; epothilone biosynthesis; thiazole ring formation; taxol substitute;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetase EPOS P, which is one of several epothilone biosynthetic enzymes encoded by a 68.75 kb contig. Epothilones A and B are 16-membered macrocyclic polyketides with an acylcysteine-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a Sorangium cellulosum non-ribosomal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page 109-113; 174pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated epothilone synthase genes, used for the recombinant production of epothilone for use in cancer therapy \,\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ55887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-1998;
24-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                 used for the recombinant production of epothilones in a heterologous host that is more amenable to fermentation.
                                                                                                                                                                                                                                                                                                                                               Sequence
29-AUG-2001
                                         AAU02010;
                                                                              AAU02010 standard; Protein; 75 AA.
                                                                                                                                                                                  474 LLDDMLEA 481
                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                       2 LXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-097741/08.
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                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                   1410 AA;
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0099504.
98US-0101631.
99US-0118906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-EP04171.
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molnar I,
                                                                                                                                                                                                                                                                                        78.9%;
75.0%;
                                                                                                                                                                                                                                                                       1:
                                                                                                                                                                                                                                                                                        Score 30; DB 21;
pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zirkle R, Goerlach J,
                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                Length 1410;
                                                                                                                                                                                                                                                                             0,;
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B
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                                                                                                                                                              RESULT 25
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein; autoimmune disorder; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; angiogenesis; nervous system disorder; bacterial infection; viral infection; fungal infection; ocular disorder; wound healing; tissue regeneration; epithelial cell proliferation; skin ageing; chemotaxis; IgG Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene #37 human secreted protein homologous amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents a polypeptide homologous to a human secreted protein of the invention. Secreted proteins and their related nucleic acids can be used in the diagnosts of or susceptibility to a pathological condition by determining the presence or absence of a mutation in a nucleic acid or the presence or amount of expression of a secreted protein. The sequences are used to prevent, treat or ameliorate a medical protein in e.g. humans, mice, rabbits, goats, horses, cats, dogs, condition in e.g. humans, mice, rabbits, goats, horses can also be used in chickens or sheep. The antibodies to the polypeptides can also be used in alleviating symptoms associated with disorders and in diagnostic immunoassays e.g. radicimmunoassays or enzyme linked immunosorbent arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver caracteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Forty one nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-SEP-2000; 2000WO-US26324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200123598-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 511-512; 518pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-281684/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Komatsoulis G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                  liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The peptides can also be used to aid wound healing and epithelial cell proliferation, to help prevent skin ageing due to sunburn, to maintain organs before transplantation, to regenerate tissues, in chemotaxis and as a food transplantation.
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 additive or preservative to alter storage capabilities
                                                                                                                      AAG74726 standard; Protein; 97 AA.
Human colon cancer antigen protein SEQ ID NO:5490
                                                                                    AAG74726;
                                              03-SEP-2001 (first entry)
                                                                                                                                                                                                                         28 DDLLEA 33
                                                                                                                                                                                                                                                           4 DDLLEA 9
                                                                                                                                                                                                                                                                                                   Local Similarity es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    75 AA;
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0155807
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                                                                                                                                                                                                                                                                                                     76.J.
100.08; FJ
                                                                                                                                                                                                                                                                                                                               76.3%; Score 29;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA;
                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                               1.1e+02;
                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                  Length 75;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                    Gaps
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0;

Human; colon cancer; colon cancer antigen; diagnosis; detection;

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RESULT 26
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                      Query Match
                               Arabidopsis thaliana
                                                       hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                   Protein identification; signal transduction pathway; metabolic pathway;
                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 1454.
                                                                                                                            17-OCT-2000 (first entry)
                                                                                                                                                                           AAG05155 standard; Protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where cancer antigens are collectively known as colon cancer antigens. The colon therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing
                                                                                                                                                                                                                                                                                                                                                         present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and AAB37789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 7086; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAH34131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                             59 LCDDLIEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-2000; 2000WO-US26524
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                                                                                                                                                                                                                                                                                              Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                     2 LXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-235357/24.
                                                                                                                                                                                                                                                                                                                                              97 AA;
                                                                                                                                                                                                                                                                                            Conservative
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99US-0163280.
                                                                                                                                                                                                                                                                                                      76.3%;
75.0%;
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                                                                                                                                                                                                                                                                                     Score 29; DB 22; Le
Pred. No. 1.5e+02;
'Mismatches 1;
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                                                                                                                                                                                                                                                                                                              Length 97;
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                                                                                                                                                                                                                                                                                     0;
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      23-JUN-1999;
24-JUN-1999;
28-JUN-1999;
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23-JUN-1999;
                                                                                                   21-JUN-1999;
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17-JUN-1999;
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18-JUN-1999;
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18-JUN-1999;
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27-MAY-1999
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-мау-1999;
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18-MAY-1999;
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29-MAR-1999;
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99US-0140991.
99US-0141287.
99US-0141842.
                                   99US-0140353.
99US-0140354.
99US-0140695.
99US-0140823.
                                                                                                                                                                        99US-0139453
99US-0139452
99US-0139454
99US-0139455
99US-0139456
99US-0139457
99US-0139459
99US-0139460
                                                                                      99US-0139750.
99US-0139763.
99US-0139817.
99US-0139899.
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99US-0136782.
99US-0137222.
99US-0137528.
99US-0137502.
99US-0137724.
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99US-0139463.
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990S-0134216
990S-0134218
990S-0134219
990S-013471
990S-013476
990S-0134941
990S-0135124
990S-013553
990S-0135629
990S-0135629
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99US-0139452.
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99US-0138540
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99US-0132487
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99US-0132485
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99US-0130891.
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AC XXX AC

В Qγ

01-JUL-1999 02-JUL-1999 06-JUL-1999 08-JUL-1999 09-JUL-1999 12-JUL-1999 13-JUL-1999 14-JUL-1999 15-JUL-1999 16-JUL-1999

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RESULT 27
AAG05154
ID AAG055
XX AAG05
XX AAG05
XX AAG05
XX AAG05
XX AFAbi
XX Prote
KW hybri
KW termi
XX Fermi
XX AFAbi
XX EP10
XX EP10
XX EP10
XX 25-FF
XX 25-FF
                                                                                                                                                                                                                               Вþ
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                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                           Query Match
Best Local
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22-SEP-1999
23-SEP-1999
24-SEP-1999
28-SEP-1999
04-OCT-1999
06-OCT-1999
07-OCT-1999
07-OCT-1999
13-OCT-1999
13-OCT-1999
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13-OCT-1999
14-OCT-1999
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14-OCT-1999;
14-OCT-1999;
18-OCT-1999;
21-OCT-1999;
21-OCT-1999;
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22-OCT-1999;
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26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
                                                                                        protein identification; signa
hybridisation assay; genetic
termination sequence.
                                                                                                                                                                                  AAG05154 standard; Protein; 153 AA.
                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 1453.
                                                                                                                                               17-OCT-2000
                                                                                                                                                                  AAG05154;
                                                                                                                                                                                                                             4 DDLLEA 9
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13 DDLLEA 18
25-FEB-1999;
                  25-FEB-2000; 2000EP-0301439
                                    06-SEP-2000.
                                                      EP1033405-A2
                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                   Similarity 100.
6; Conservative
                                                                                                                                                                                                                                                                                                      99US-0154779
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                                                                                                                                                (first entry)
 99US-0121825
                                                                                                                                                                                                                                                                             76.3%;
                                                                                                   signal transduction pathway; metabolic pathway;
netic mapping; gene expression control; promoter;
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pred. No. 2.2e+02;
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990S-0142154.
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ABB97149
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Best Local
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06-OCT-1999;
07-OCT-1999;
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12-OCT-1999;
13-OCT-1999;
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14-OCT-1999
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14-OCT-1999;
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                                                                                                                                                     Human tumour antigen related protein SEQ ID NO 51.
                                                                                                                                                                                                   ABB97149 standard; Protein; 216 AA
                                                                                                                                       Human; tumour; antigen; HLA-A2; cytotoxic T cell; cytostatic; cancer;
                                                                                                                                                                      21-JUN-2002 (first entry)
                                                                                       07-FEB-2002.
                                                                                                     WO200210369-A1.
                                                                                                                   Homo sapiens
                                                          31-JUL-2000; 2000JP-0231814
                                                                        30-JUL-2001; 2001WO-JP06526
       N-PSDB; ABL56077
              WPI; 2002-291857/33.
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                                                                                                                                                                                                                                                     4 DDLLEA 9
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                     Conservative
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990S-0160814
990S-0160815
990S-0160980
990S-0160980
990S-0161404
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99US-0159294.
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99US-0160767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a peptide comprising an amino acid sequence selected from 44 fully defined amino acid sequences (ABB969549)6-ABB969549) and a polypeptide comprising an amino acid sequence selected from the 9 fully defined amino acid sequences (ABB97147-ABB97151). The above comprise a tumour antigen inducing or activating HLA-A2-restricted tumour-specific cytotoxic T cells, which recognise HLA-A2 and a tumour antigen peptide and is thus activated. The peptides and polypeptides have cytostatic activity. The tumour antigen is useful in diagnosis of and screening drugs for specific treatment of pancreatic cancer, colon and screening drugs for specific treatment of pancreatic cancer. The present cancer and stomach cancer including in the form of vaccines. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor antigens inducing and/or activating HLA-A2-restricted tumor-specific cytotoxic T cells, useful in diagnosis of and screening drugs e.g. cancer vaccines for specific treatment of pancreatic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence is that of a tumour antigen protein, useful to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG21583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG21583 standard; Protein; 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #21574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-2002 (first entry)
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess because the contract of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 IILDDLLE 208
                                                                                                                                                                                               Claim 20; SEQ ID No 51942; 103pp; English.
                                                                                                                                                                                                                                                              biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS85770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VLXDDLLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Page 107-108; 127pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           υ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.3%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB
Pred. No. 3.4e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT 30
ANG 57749
ID ANG 57749
ACC ANG 577
XX ANG 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for identifying expressed genes. (I) is useful in gene therapy techniques (C (II), (II) is useful for generating antibodies against it, detecting or guantitating a polypeptide in tissue, as molecular weight markers and as c imaging of sites expressing (II) and (II) are useful in medical c imaging of sites expressing (II). (I) and (II) are useful in medical c imaging of sites expressing (II). (I) and (II) are useful for treating c The polypeptide and polynucleotide sequences have applications in c diagnostics, forensics, gene mapping, identification of mutations c responsible for genetic disorders or other traits to assess blodiversity amino acid sequences. ABG00010-ABG30377 represent novel human c diagnostic amino acid sequences of the invention.

CC specification, but was obtained in electronic format directly from WIPO cat fire wide, but was obtained and port seminances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                     23-MAR-1999
25-MAR-1999
29-MAR-1999
01-APR-1999
06-APR-1999
16-APR-1999
16-APR-1999
21-APR-1999
21-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
30-APR-1999
04-MAY-1999
06-MAY-1999
06-MAY-1999
                                                                                                                                                                                                                                                                                                                                  25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 74457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG57749 standard; Protein; 224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG57749;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 VINDDVIEA 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
                                                                                                                                                                                                                                                                                                                                                                                             2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                  99US-0126264
99US-012785
99US-0127462
99US-0128234
99US-0128234
99US-0130077
99US-0130077
99US-0130510
99US-0130510
99US-0132048
99US-0132486
99US-0132486
99US-0132486
99US-0132863
99US-0132863
                                                                                                                                                                                                                                                                                                                99US-0123180.
99US-0123548.
99US-0125788.
                                                                                                                                                                                                                                                                                                                                                              99US-0121825
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55.6%;
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Pred. No. 3.5e+
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.5e+02;
1;
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        20-JUL-1999
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21-JUL-1999
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22-JUL-1999
22-JUL-1999
23-JUL-1999
23-JUL-1999
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19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
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19-JUL-1999;
19-JUL-1999;
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21-JUN-1999
22-JUN-1999
23-JUN-1999
23-JUN-1999
24-JUN-1999
24-JUN-1999
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01-JUL-1999;
02-JUL-1999;
06-JUL-1999;
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14 -MAY 1999
14 -MAY 1999
14 -MAY 1999
19 -MAY 1999
19 -MAY 1999
20 -MAY 1999
21 -MAY 1999
21 -MAY 1999
25 -MAY 1999
25 -MAY 1999
27 -MAY 1999
01 -JUN-1999
01 -JUN-1999
01 -JUN-1999
10 -JUN-1999
11 -JUN-1999
                                                                                                                                                                            20-JUL-1999
                                                                                                                                                                                                                                                                                                      16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-1999;
99US-0140991.
99US-0141287.
99US-0141287.
99US-0142154.
99US-0142390.
99US-014297.
99US-014354.
99US-0144005.
99US-0144005.
99US-0144086.
99US-014433.
99US-014433.
99US-014433.
99US-014433.
99US-014433.
99US-014433.
99US-014433.
99US-014438.
99US-014438.
99US-014438.
99US-014508.
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99US-0140695.
99US-0140823.
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990S-0139454
990S-0139455
990S-0139456
990S-0139456
990S-0139461
990S-0139461
990S-0139461
990S-0139462
990S-0139463
990S-0139763
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990S-0139763
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990S-0139763
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99US-0134219

99US-0134221

99US-0134768

99US-0134941

99US-0135124

99US-0135629

99US-0135629

99US-0136021

99US-0136782

99US-013722

99US-0137724

99US-0137724

99US-0137724

99US-0137724

99US-0138440

99US-0138847

99US-0139453
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23-JUL-1999 26-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 02-AUG-1999 02-AUG-1999 02-AUG-1999 04-AUG-1999 04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999

99US-0145919. 99US-0145951. 99US-0146386. 99US-0146388. 99US-0146389. 99US-0147038. 99US-0147204.

99US-0145224. 99US-0145276. 99US-0145913.

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RESULT 31
ABB54117
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Best Local :
                        Query Match
Best Local S
Matches 6
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28-OCT-1999;
29-OCT-1999;
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25-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
                                                                                                           The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB5300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent wo200177334 (published 18-0CT-2001) which is available in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FR2807446-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB54117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB54117 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                    (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2000; 2000FR-0004630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis IL1403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis protein yibB
                                                                                                                                                                                                                                                                             \ensuremath{\mathsf{New}} nucleotide sequence useful in the identification or Lactococcus lactis and related species -
                                                                                                                                                                                                                                                                                                                     WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                               Bolotine A,
                                                                                                                                                                                                                                                       Claim 6; SEQ ID No 819; 2504pp; French.
                                                                          Sequence
                                                                                                  format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VLXDDLLE 8
                        Local Similarity
les 6; Conserv
 4 DDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLIDDLLE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                            244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                               Sorokine A, Renault P, Ehrlich
                            Conservative
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99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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99US-0161404.
99US-0161405.
99US-0161406.
99US-0161359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.3%;
75.0%;
                                       76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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pred. No. 3.5e+02; 
1; Mismatches 1; Indels
                                        Score 29; pred. No.
                             0;
                             Mismatches
                                                     DB 23;
                                           3.9e+02;
                                                     Length 244;
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                0;
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                                Gaps
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20-AUG-1999; 23-AUG-1999; 23-AUG-1999; 25-AUG-1999; 25-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999;

30-AUG-1999; 31-AUG-1999; 01-SEP-1999; 07-SEP-1999;

10-SEP-1999; 13-SEP-1999; 15-SEP-1999;

16-SEP-1999;

24-SEP-1999; 28-SEP-1999; 29-SEP-1999; 04-OCT-1999; 05-OCT-1999; 06-OCT-1999; 07-OCT-1999;

990S-0155486. 990S-0156458. 990S-0156458. 990S-0156459. 990S-0157117. 990S-0157753. 990S-0157755. 990S-0158029. 990S-01580232.

08-OCT-1999; 12-OCT-1999; 13-OCT-1999;

99US--S066 -S066 -S066

of

0;

13-OCT-1999; 13-OCT-1999; 14-OCT-1999;

14-OCT-1999; 14-OCT-1999;

14-0CT-1999 14-0CT-1999 18-0CT-1999 21-0CT-1999 21-0CT-1999 21-0CT-1999 21-0CT-1999 21-0CT-1999 21-0CT-1999 21-0CT-1999 22-0CT-1999 22-0CT-1999

990S-0159294 990S-0159295 990S-0159329 990S-0159330 990S-0159330 990S-015953 990S-015958 990S-0160741 990S-0160767 990S-0160770 990S-0160770 990S-0160814 990S-0160814 990S-0160881

20-SEP-1999; 22-SEP-1999; 23-SEP-1999;

16-AUG-1999; 17-AUG-1999; 18-AUG-1999; 20-AUG-1999; 20-AUG-1999;

990S-0147302.
990S-014716.
990S-0147303.
990S-0147493.
990S-014811.
990S-0148341.
990S-0149368.
990S-0149426.
990S-0149722.
990S-0149723.
990S-0149723.
990S-0149902.
990S-0151066.
990S-0151066.
990S-0151066.
990S-0151066.
990S-0151066.
990S-0151066.
990S-0151066.

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RESULT 32
AAG57748
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
23-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thaliana protein fragment SEQ ID NO:
            99US-0129845

99US-0130449

99US-0130449

99US-0132486

99US-0132486

99US-0132486

99US-0132486

99US-0132486

99US-0132486

99US-0134286

99US-0134218

99US-0134219

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99US-0139642
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      23 JUL-1999
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28 JUL-1999
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99US-0139463.
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99US-0142184.
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99US-0145918.
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99US-0147403.
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RESULT 33
AAB60860
ID AAB60
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Best Local S
Matches 6
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18-AUG-1999
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31-AUG-1999
31-AUG-1999
31-AUG-1999
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22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
07-OCT-1999;
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13-SEP-1999
AAB60860 standard; protein; 292 AA
                                  34 LLIDDLLE 41
                                              1 VLXDDLLE 8
                                                            Similarity 6; Conserv
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0149175.
99US-0149426.
99US-0149722.
99US-0149723.
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99US-0157753
99US-0157865
99US-0158029
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99US-0169741
99US-01607741
99US-01607741
99US-01607770
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99US-0151303.
99US-0151438.
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99US-0150566.
99US-0150884.
99US-0151065.
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99US-0156458.
99US-0156596.
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99US-0161405.
99US-0161406.
99US-0161359.
99US-0161360.
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99US-0160815.
99US-0160980.
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99US-0154039.
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                                                                                                                                                         99US-0160981.
99US-0160989.
                                                                                                    99US-0161920.
99US-0161992.
                                                                                                                  99US-0161361
                                                                                       99US-0161993.
99US-0162142.
                                                                  76.3%;
75.0%;
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                                                                   Score 29; DB 21;
Pred. No. 4e+02;
                                                              Mismatches
                                                                          Length 249;
                                                              Indels
                                                              0;
                                                             Gaps
                                                               0,
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RESULT 34
ABP28408
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 Best Local Similarity Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-1999;
02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mevalonate pathway protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB60860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200078935-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mevalonate pathway; disease; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brown JR, 'Wilding EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-2000; 2000WO-US17262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to an isolated mevalonate pathway gene derived from a bacterium from clade of Class II of the phylogenetic tree referred to in the specification. The invention may used for treatment of disease related to bacterial infection, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-071392/08
                                                                                                                                                    Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conjunctivitis, pneumonia, bacteremia and meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 14; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated mevalonate pathway gene polynucleotide derived bacterium is useful for treatment of bacterial infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                  ABP28408;
                                                                                                                                                                                                                   Streptococcus polypeptide SEQ ID NO 5992.
                                                                                                                                                                                                                                                                                                                ABP28408 standard; Protein; 297
                                                             02-MAY-2002
                                                                                                                         Streptococcus pyogenes.
                                                                                                                                                                                                                                                    02-JUL-2002 (first entry)
27-OCT-2000; 2000GB-0026333
                             29-OCT-2001; 2001WO-GB04789.
                                                                                             WO200234771-A2
                                                                                                                                                                                                                                                                                                                                                                                              111 LSDDLLE 117
                                                                                                                                                                                                                                                                                                                                                                                                                          2 LXDDLLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gwynn M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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99US-0146682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mathie TB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29; DB 22;
Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 292;
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B
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                                                                                                                                                                                                                                                                                            RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a protein (ABP25413-ABP30895) from group B CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (31), given in CC the specification. The proteins have antibacterial and antiinflammatory CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and CC antibodies that bind (I) are used in the manufacture of medicaments for CC the treatment or prevention of infection or disease caused by CC streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. CC Nucleic acids encoding (I) are used to detect Streptococcus in a CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to determine whether a compound binds to CC (I). A composition or diagnostic composition. The disease caused by CC streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be conformatography, immunoassays, and distinguishing/identifying treptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
           25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
                                                                  25-FEB-2000;
                                                                                                                                  Arabidopsis thaliana
                                                                                        06-SEP-2000
                                                                                                             EP1033405-A2
                                                                                                                                                         termination sequence
                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 999.
                                                                                                                                                                                                                          17-OCT-2000
                                                                                                                                                                                                                                                                    AAG04826 standard; Protein; 358
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 3761; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                            116 LSDDLLE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Telford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                   297 AA;
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                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                       (first entry)
                                                                2000EP-0301439
          99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
                                                                                                                                                                                                                                                                                                                                                                              76.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                  Score 29; DB 23; I
Pred. No. 4.8e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                        Length 297;
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                                                                                                                                                                                                                                                                                                                                                                   0;
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    02-JUL-1999;
06-JUL-1999;
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   13-JUL-1999;
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16-JUL-1999;
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10-JUN-1999;
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29-MAR-1999
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14-MAY-1999
99US-0140991
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99US-0141842
99US-0142154
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99US-014362
99US-014362
99US-014368
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99US-0139763.
99US-0139817.
99US-0139899.
99US-0140353.
99US-0140695.
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990S-0137528

990S-0137520

990S-0138094

990S-013804

990S-013804

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990S-0139452

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990S-0139454
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9908-0135629.
9908-0136021.
9908-0136392.
9908-0136782.
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99US-0139461
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99US-0134941.
99US-0135124.
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99US-0134256.
99US-0134218.
99US-0134219.
99US-0134221.
99US-0134370.
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99US-0132048.
99US-0132407.
99US-0132484.
99US-0132484.
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99US-0139457
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99US-0129845.
99US-0130077.
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99US-0126785.
99US-0127462.
99US-0128234.
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99US-0130891.
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   RESULT 36
AAG61479
ID AAG61
XX AG61
XX AG61
XX Prote
XX Prot
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Matches 6
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25-FEB-1999

05-MAR-1999

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23-MAR-1999

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01-APR-1999

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12-OCT-1999;
13-OCT-1999;
                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG61479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 79746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG61479;
                                                                                                                                                                                              25-FEB-2000;
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6; Conserv
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                                                                                                                                                                                              2000EP-0301439
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990S-0159294

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990S-0159330

990S-0159331

990S-0159584

990S-0160741

990S-0160767

990S-0160768

990S-0160768

990S-0160768

990S-0160814

990S-0160814

990S-016081

990S-0161406

990S-0161406

990S-0161405

990S-0161405

990S-0161351

990S-0161351

990S-0161932

990S-0161932
99US-0121825.
99US-0123180.
99US-012548.
99US-0125788.
99US-0126785.
99US-0126785.
99US-0128746.
99US-0128234.
99US-0128234.
99US-0128814.
99US-0128874.
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75.0%;
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Pred.
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red. No. 5.8e+02;
Mismatches 1;
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promoter;

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99US-0134941 99US-0135124 99US-0135333 99US-0135333 99US-0135722 99US-0137528 99US-0137528 99US-0137528 99US-0138447 99US-0138447 99US-0139453 99US-0139453 99US-0139458 99US-0139459 99US-0139459 99US-0139459 99US-0139461 99US-0139461 99US-0139463 99US-014095 99US-014233	99US-0130449 99US-01308510 99US-0131449 99US-0132048 99US-0132487 99US-0132485 99US-0132486 99US-0132486 99US-0132486 99US-0134286 99US-0134218 99US-0134219 99US-0134219 99US-0134219 99US-0134219
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14-OCT-1999;
14-OCT-1999;
18-OCT-1999;
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                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                    WPI; 2001-639362/73.
N-PSDB; AAS93903.
                                                                                                                                                                                                                                                 WO200175067-A2
                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #29707.
                                                                                                                                                                                                                                                                                                                                          18-FEB-2002 (first entry)
polypeptide (II) sequences. (I) is useful as hybridisation
                                                                                                                                                                           31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                              11-OCT-2001
                                                                                                                                                                                                                                                                      Homo sapiens.
           The invention relates to isolated polynucleotide (I) and
                              Claim 20; SEQ ID No 60075; 103pp; English
                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                            2000US-0649167
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99US-0159584.
99US-0160741.
99US-0160767.
99US-0160768.
99US-0160770.
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990S-0161360.
990S-0161361.
990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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99US-0160815.
99US-0160980.
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99US-0160989.
99US-0161404.
99US-0161405.
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99US-0159637.
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75.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
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les 1;
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   probes,
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RESULT 38
AAB94128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful in gene therapy techniques CC to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.
Matches
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                                                                                                                                                                                                                                                                                                           29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein sequence SEQ ID NO:14383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB94128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB94128 standard; Protein; 405 AA.
                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection, and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-2001 (first entry)
                                                 Claim 8; SEQ ID 14383; 2537pp + CD ROM; English.
                                                                                                                                                                                  WPI; 2001-318749/34.
                                                                                                                                                                                                                                      Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                        (HELI-) HELIX RES INST.
                                                                                      full-length cDNAs
                                                                                                                                                                                                                     Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 LGDDVLEA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                      Isogai T,
                                                                                                                                                                                                                 sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396 AA;
                                                                                                                                                                                                                                                                                                             ; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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75.0%;
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Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 29; DB 22;
Pred. No. 6.4e+02;
1; Mismatches 1
                                                                                                                                                                                                                      Saito K, Yamamoto J;
(, Otsuki T;
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set

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RESULT 39
AAG04825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary CC to the 502 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprises as the comprise which comprises a 5'-end complementary to the CC opinucleotide which comprises as 3'-end sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC the full-length cDNAs. The primers are also useful for the CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB13633 to AAH18742 represent human cDNA sequences; AAB92446 to CC AAB95893 represent human amino acid sequences; AAB92446 to AAH3629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG04825 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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153 ILLDDLSEA 161
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nes 6; Conserv
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      99US-0126264

99US-0126785

99US-0127462

99US-0128234

99US-0128714

99US-0130077

99US-0130070

99US-0130449

99US-0130891

99US-0131449

99US-0132484

99US-0132484

99US-0132485
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99US-0123548.
99US-0125788.
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66.7%;
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Pred. No. 6.6e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                         mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 405;
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18 -MAY 1999
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06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
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13-JUL-1999;
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28-JUN-1999;
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14-MAY-1999
           99US-0140823

99US-0141847

99US-0141842

99US-0142184

99US-0142055

99US-014205

99US-014290

99US-014392

99US-014392

99US-0143624

99US-0144085

99US-0144086

99US-0144335

99US-0144335

99US-0144335

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99US-0137502
99US-0137502
99US-0138094
99US-0138840
99US-0138847
99US-0139452
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99US-0139458
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99US-0139460.
99US-0139461.
99US-0139462.
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99US-0135629.
99US-0136021.
99US-0136392.
99US-0136782.
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99US-0134221.
99US-0134370.
99US-0134768.
99US-0134941.
99US-0135124.
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99US-0140695
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99US-0140353
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99US-0134218.
99US-0134219.
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99US-0132863.
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Best Loc
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21-OCT-1999;
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26-OCT-1999;
26-OCT-1999;
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29-OCT-1999;
25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
01-APR-1999;
16-APR-1999;
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21-APR-1999;
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30-APR-1999;
30-APR-1999;
30-APR-1999;
10-MAY-1999;
11-MAY-1999;
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hybridisation assay; genetic mapping; gene e
                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-2000
                                                                                                                                                                                                                                                                                                                        EP1033405-A2
                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                               termination
                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis
                                                                                                                                                                                                                                                                               25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VLXDDLLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 75.0
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                               on assay; on sequence.
                                                                                                                                                                                                                                                                                                                                                                                                     thaliana protein fragment SEQ ID NO: 79745.
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0160814
99US-0160815
99US-0160980
99US-0160981
99US-0160989
99US-0161405
99US-0161406
99US-0161350
99US-0161360
99US-0161360
99US-0161920
99US-0161922
99US-0161922
99US-0161923
                                                                                                                                                                                                                                                                               2000EP-0301439
   990S-0121825

990S-012548

990S-0125788

990S-0125785

990S-0126264

990S-0127862

990S-0128714

990S-0128714

990S-0128714

990S-0130077

990S-0130497

990S-0130491

990S-0131449

990S-0132486

990S-0132486

990S-0132485

990S-0132485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                        genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29; DB 21;
pred. No. 6.7e+02;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 AA
                                                                                                                                                                                                                                                                                                                                                                                       pathway; metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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22-JUL-1999;
22-JUL-1999;
23-JUL-1999;
23-JUL-1999;
23-JUL-1999;
26-JUL-1999;
27-JUL-1999;
27-JUL-1999;
27-JUL-1999;
27-JUL-1999;
28-JUL-1999;
28-JUL-1999;
29-AUG-1999;
30-AUG-1999;
30-AUG-1999;
31-AUG-1999;
31-AU

990S-0145089.
990S-0145185.
990S-0145218.
990S-0145218.
990S-0145218.
990S-0145218.
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990S-0145218.
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990S-0145218.
990S-0145218.
990S-0146388.
990S-0147302.
990S-0147303.
990S-0147260.
990S-0147260.
990S-0147416.
990S-014726.
990S-014726.
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990S-014936.
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990S-01551065.
990S-0155036.

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05-AUG-1999 06-AUG-1999 06-AUG-1999 06-AUG-1999 10-AUG-1999 11-AUG-1999 11-AUG	6661 6661 6661 6661 6661 6661
99US-0147303 99US-0147192 99US-0147260 99US-0147260 99US-0147416 99US-0147416 99US-0148311 99US-0148311 99US-0148368 99US-0149723 99US-0149723 99US-0149723 99US-0150864 99US-0150866 99US-0150866 99US-0151080 99US-0151303 99US-0151303 99US-0151303 99US-0154783 99US-0154784 99US-015479 99US-0158846 99US-0158869 99US-01593758 99US-01593758 99US-01593758 99US-015965 99US-015965 99US-015965 99US-0159753 99US-015965 99US-0159753 99US-0159753 99US-0159753 99US-015965 99US-015965 99US-015965 99US-015965 99US-015965 99US-015965 99US-015965 99US-015965 99US-0159676 99US-0159637 99US-0159637 99US-0160768 99US-0160768 99US-0160768 99US-0160881 99US-0160881	0145 0145 0145 0146 0146 0146 0147

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AAG04824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
26-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
21-APR-1999;
21-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG04824 standard; Protein; 415 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VLXDDLLE 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0161406
99US-0161369
99US-0161360
99US-0161361
99US-0161920
99US-0161920
99US-0161993
99US-0162142
99US-0121825.
99US-0123548
99US-0123548
99US-0125788
99US-0126785
99US-0127462
99US-0120045
99US-0130049
99US-0130049
99US-013049
99US-0131449
99US-0132486
99US-0132486
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99US-0132486
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99US-0134218
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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        27 - MAY - 1999;
28 - MAY 1999;
01 - JUN - 1999;
03 - JUN - 1999;
07 - JUN - 1999;
07 - JUN - 1999;
10 - JUN - 1999;
10 - JUN - 1999;
11 - JUN - 1999;
16 - JUN - 1999;
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17 - JUN - 1999;
18 - JUN - 1999;
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08-JUL-1999;
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15-JUL-1999;
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990S-0145086
990S-0145086
990S-0145086
990S-0145086
990S-0145086
990S-0145388
990S-0145913
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99US-0136782.
99US-0137222.
99US-0137528.
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04-AUG-1999 04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999 09-AUG-1999

-AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999;

Length 415;

0;

Gaps

0;

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99US-0158369
99US-0158369
99US-0159294
99US-0159294
99US-0159330
99US-0159330
99US-0159638
99US-0159638
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99US-0160815
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99US-0161360
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99US-0161361
                                                                                                                                                                                                                                                                                                                                                                               990S-0147303
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990S-014992
990S-014992
990S-0150566
990S-015066
990S-015075
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99US-0147302.
99US-0147192.
99US-0147260.
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S-0156596.
S-0157117.
S-0157753.
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    RESULT 42
AAG61477
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Best Local
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 20-MAY-1999
21-MAY-1999
24-MAY-1999
25-MAY-1999
27-MAY-1999
27-MAY-1999
01-JUN-1999
01-JUN-1999
04-JUN-1999
07-JUN-1999
                                                                                                                  28-APR-1999
30-APR-1999
30-APR-1999
04-MAY-1999
05-MAY-1999
06-MAY-1999
06-MAY-1999
11-MAY-1999
11-MAY-1999
14-MAY-1999
14-MAY-1999
14-MAY-1999
14-MAY-1999
14-MAY-1999
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08-APR-1999
16-APR-1999
19-APR-1999
21-APR-1999
23-APR-1999
23-APR-1999
                                                                                                                                                                                                                                                                                                                                                    05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG61477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG61477 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thaliana protein fragment SEQ ID NO: 79744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
99US-0132484

99US-0132485

99US-0132487

99US-013283

99US-013425

99US-0134218

99US-0134221

99US-0134221

99US-013476

99US-0134941

99US-0135124

99US-013523

99US-0137528

99US-0137528

99US-0137528

99US-0137528

99US-0137528
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99US-0132048.
99US-0132407.
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99US-0130891.
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99US-0129845.
99US-0130077.
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99US-0125788.
99US-0126264.
99US-0126785.
99US-0127462.
99US-0128234.
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99US-0123180
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 415 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29; DB;
Pred. No. 6.7e-
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
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24-SEP 1999 28-SEP 1999 29-SEP 1999 29-SEP 1999 04-OCT 1999 05-OCT 1999 07-OCT 1999 07-OCT 1999 12-OCT 1999 13-OCT 1999

-S066 -S066 -S066 99US-99US 10-AUG-1999
11-AUG-1999
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13-AUG-1999
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14-AUG-1999
17-AUG-1999
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13-OCT-1999 13-OCT-1999 14-OCT-1999 14-OCT-1999 14-OCT-1999 14-OCT-1999 14-OCT-1999 14-OCT-1999 21-OCT-1999 22-OCT-1999 22-OCT-1999 23-OCT-1999 25-OCT-1999 25-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 26-OCT-1999 27-OCT-1999 28-OCT-1999 28-OCT-1999 28-OCT-1999 28-OCT-1999 28-OCT-1999

Query Match  Best Local Simila  Matches 6; Cc  Qy 1 VLXDDLLE	PR 29-OCT-199	PR 28-0CT-199 PR 28-0CT-199 PR 28-0CT-199	PR 26-OCT-199 PR 26-OCT-199	PR 25-OCT-199	PR 25-0CT-1999	PR 22-0CT-1999	PR 21-OCT-1999 PR 21-OCT-1999	PR 21-0CT-1996 PR 21-0CT-1996	PR 18-OCT-1999 PR 21-OCT-1999 PR 21-OCT-1999	PR 14-OCT-1999 PR 14-OCT-1999	PR 14-OCT-1999 PR 14-OCT-1999	PR 13-0CT-1999 PR 14-0CT-1999	PK 13-OCT-1999 PR 13-OCT-1999 PR 13-OCT-1999	PR 07-OCT-1999 PR 08-OCT-1999	PR 04-0CT-1999 PR 06-0CT-1999	PR 28-SEP-1999 PR 29-SEP-1999	PR 23-SEP-1999, PR 24-SEP-1999	PR 16-SEP-1999 PR 20-SEP-1999 PP 22-SEP-1999	PR 10-SEP-1999; PR 15-SEP-1999; PR 15-SEP-1999;	PR 01-SEP-1999; PR 07-SEP-1999	PR 30-AUG-1999; PR 31-AUG-1999;	PR 27-AUG-1999;	PR 25-AUG-1999; PR 25-AUG-1999;	PR 23-AUG-1999; PR 23-AUG-1999;	PR 20-AUG-1999;	PR 17-AUG-1999; PR 18-AUG-1999;	PR 13-AUG-1999; PR 16-AUG-1999;	PR 12-AUG-1999; PR 13-AUG-1999;
)0.3 Similarity 75.08 Conservative	99US-	-S066 -S066	-S066 -S066	-S066 -S066	-SD66 -SD66	-SU66 -S066	-Sn66 -Sn66	-S066 -S066	-Suse -Suse -Suse -Suse	-S066	99US-1	99US-(	-S066 -S066	)-Sil66 )-Sil66 )-Sil66	)-S066	0-8066 0-8066	99US-0	0-8066 0-8066 0-8066	9; 99US-0153758. 9; 99US-0154018.	0-SU66 0-S066	99US-0	0-SD66	99US-0	99US-01	99US-01	99US-01	99US-01	99US-01 99US-01

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ABB67967
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ID ABB
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Drosophila melanogaster polypeptide SEQ ID NO 30693
                                   26-MAR-2002
                                                                           ABB67967 standard; Protein; 468 AA
                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventifuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLO1840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                            specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed
                                                                                                                                                385 IIGDDIIEA 393
                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 24720; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 24720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB65976 standard; Protein; 429 AA
                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB65976;
                                                                                                                                                                       1 VLXDDLLEA 9
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66 LLIDDLLE 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL10079
                                                                                                                                                                                                                                                 429 AA;
                               (first entry)
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-191637P
                                                                                                                                                                                                            44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection reagent for detecting 1000 or more
                                                                                                                                                                                                       Score 29; DB 22
Pred. No. 7e+02;
                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                 Length 429;
                                                                                                                                                                                         Indels
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Best Local Similarity
Grandes 6; Conserv:
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                                                                                                                                                                                                                                                                                                                                   RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                             23-MAR-2001; 2001WO-US09231.
23-MAR-2000; 2000US-191637P.
                                                                                              W0200171042-A2
                                                                                                                          Drosophila melanogaster.
                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 28287.
                                                                                                                                                                                                                                                                       ABB67165;
                                                                                                                                                                                                                                                                                             ABB67165 standard; Protein; 505 AA.
                                                                                                                                                                                                                                      26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLOBA) ABLI6175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 30693; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABL12070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                            92 VLLDDLLQ 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                            1 VLXDDLLE 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468 AA;
                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-191637P.
2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 46
AAB10764
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable of detecting 1000 or more genes from Drosophila. The inventue useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176 ABLIG176 ABLIG171), expressed DNA sequences (ABLIG1840-ABLIG175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 28287; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                 T gene; human; central nervous system development; CNS; nootropic; neuroleptic; antidepressant; gene therapy; antisense; treatment; schizophrenia; autism; manic depression; mental retardation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB10764 standard; Protein; 542 AA.
                                                                                                                                                                                                                                                                                                                                                                           Human T protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB10764;
                                                                                                                                                                                                                                                             DE19908423-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 VLLDDLLQ 113
                                                                                                                                                                           26-FEB-1999;
                                                                                                                                                                                                    26-FEB-1999;
                                                                                                                                                                                                                                31-AUG-2000
                                                                                                                                                                                                                                                                                       Homo sapiens.
            system (CNS), antisense sequences, ribozymes and antil treatment of, e.g. schizophrenia and manic depression {\bf r}
                        DNA encoding a protein involved in development of the central nervous system (CNS), antisense sequences, ribozymes and antibodies, useful f
                                                                         N-PSDB; AAA98006
                                                                                       WPI; 2000-580150/55.
                                                                                                                Poustka A,
                                                                                                                                            (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                  Coy J;
                                                                                                                                                                           99DE-1008423.
                                                                                                                                                                                                      99DE-1008423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29; I
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                    for
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Дb

Sequence

542 AA;

0;

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CC describes a method for producing (1) antisense RNA that is complementary to DNA as above, which can reduce or inhibit synthesis of the protein CC coding DNA; (2) a ribozyme, which is complementary to DNA as above, which can reduce or inhibit synthesis of the protein CC specifically binds to and cleaves transcribed DNA, which reduces or CC inhibits synthesis of the protein coding DNA; (3) an expression vector, CC containing DNA as above, or which encodes antisense RNA or a ribozyme; CC encoded by DNA as above; (6) a method to produce the protein of (5); (8) a diagnostic method to produce the protein of (5); (8) a diagnostic method to detect disturbed expression of the CC contain; (7) an antibody targeted against the protein of (5); (8) a diagnostic method to detect disturbed expression of the CC contact, and comparing the expression of the protein by contacting a protein; (9) a diagnostic kit to perform the method of (8); (10) a conhaman transgenic animal, where the naturally occurring T gene has an CC altered gene structure or sequence; and (11) a method to produce a CC protein (TP) which is involved in development of the central nervous system. Antisense sequences, ribozymes and antibodies are useful for CC depression and mental retardation. This sequence represents a fragment of CC the human T protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel DNA sequence, which encodes a protein that is involved in development of the central nervous system (CNS) and has tissue and development-specific expression. The products of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 11; 86pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention have nootropic, neuroleptic and antidepressant activity and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The method also
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AAE07054
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE07054 standard; Protein; 547 AA.
                                                                                                                                                                                                                                                                                                                                                  Human secreted protein; proliferative disorder; cancer; tumour
                                                                                                                                                                                                                                                                                                                                                                                                   Human gene 4 encoded secreted protein HSYAB05, SEQ ID NO:71.
                                                                                                                                                                                                  parkinson's disease; cognitive disorder; schizophrenia; asthma;
skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
cardiovascular disorder; angiogenic disorder; kidney disorder;
                                                                                                                                                                                                                                                                        foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE07054;
                                                                                                                          endocrine disorder; infection; wound healing; vulnerar cell culture; chemotaxis; food additive; gene therapy;
                                                                                                                                                     gastrointestinal disorder; pregnancy-related disorder;
endocrine disorder; infection; wound healing; vulnerar
                                                                                                binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 ILLDDLSEA 298
                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VLXDDLLEA 9
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.3%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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WO200154708-A1

Protein

/label= Signal_peptide
16..547

/label=

Mature_human_secreted_protein

Peptide

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                                                                                              ABG65102
                                                                                                           RESULT 48
                                                                                                                                                                                                                                                                                                                           cc skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cc cardiovascular disorders, angiogenic disorders, kidney disorders, cc gastrointestinal disorders, pregnancy related disorders, endocrine cd disorders, and infections. The proteins can also be used to aid wound company and epithelial cell proliferation, to prevent skin aging due to coulture of primary tissues, to regenerate tissues, to identify their cc cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Cc antibodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked cc in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked cc secreted protein of the invention.
                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                      Query Match
   27-AUG-2002
                                                                  ABG65102 standard; Protein; 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 22 genes, based on the tissues in which they are most highly expressed, proliferative disorders, cancer, tumours, foetal and developmental abnormalities, hammatopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis) inflammation, parkinson's disease, cognitive disorders, schizophrenia, asthma, asthma, skin disorders (e.g., Alzheimer's disease).
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                              169 DDLLEA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD13345-AAD13401 represent cDNAs corresponding to 22 human secreted protein genes, and AAE07051-AAE07105 represent the proteins they encode AAE07106-AAE07129 represent human secreted protein fragments or variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The genes and their secreted proteins are useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 489-491; 558pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2000;
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                                                                                                                                                                                                4 DDLLEA 9
                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-488743/53.
                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PA, Wei P, Ebner R, Ruben SM, Barash SC;
                                                                                                                                                                                                                                                                                                        547 AA;
(first entry)
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Komatsoulis GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 2000US-0180628.
; 2000US-0226279.
; 2000US-0251988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001us-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US01434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0179065
                                                                                                                                                                                                                                                   76.3%;
100.0%;
                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                 Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker KP,
Duan DR,
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                               DB 22; Length 547; 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birse CE, Sopper Shi Y, Choi GH,
                                                                                                                                                                                                                              0,
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XXX DXXX
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                                                                                                                                                                           RESULT 49
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local
Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                       Human protein sequence SEQ ID NO:18695.
                                                                                                                                     AAB95765 standard; Protein; 559 AA
                                                                           26-JUN-2001
                                                                                                           AAB95765;
                                                                                                                                                                                                                                                                                                                                                                              encephalomyelitis, meningitis, schizophrenia), and connective (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent fusion proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to albumin fusion proteins comprising a therapeutic protein x and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                       169 DDLLEA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1750-1752; 2102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        albumin fused to a therapeutic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion protein for treating disease e.g. diabetes comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-010886/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-2000; 2000US-256931P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-APR-2001; 2001WO-US11988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer;
                                                                                                                                                                                                                                                                                       Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human albumin fusion protein #1777.
                                                                                                                                                                                                                                                        4 DDLLEA 9
                                                                                                                                                                                                                                                                                                                                                     547 AA;
                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haseltine WA;
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-229358P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-199384P
                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                   76.3%; Score 29; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                  DB 23;
                                                                                                                                                                                                                                                                                               9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                           and connective disorders
                                                                                                                                                                                                                                                                                                               Length 547;
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AAB10765
ID AAB
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XEXEX
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence's rend sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                               AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAB03166 to AAB13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID 18695; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999;
                Murine T gene protein fragment.
                                                    26-JAN-2001 (first entry)
                                                                                        AAB10765;
                                                                                                                          AAB10765 standard; Protein; 565 AA
                                                                                                                                                                                                                 307 ILLDDLSEA 315
                                                                                                                                                                                                                                                                                   Local Similarity es 6; Conserv
                                                                                                                                                                                                                                                     1 VLXDDLLEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                             559 AA;
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99ЛР-0248036
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                                                                                                                                                                                                                                                                                                        76.3%;
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                                                                                                                                                                                                                                                                                                      Score 29; DB 22;
Pred. No. 9.2e+02;
                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito K, Y, Otsuki T;
                                                                                                                                                                                                                                                                                                                           Length 559;
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313 ILLDDLSEA 321

1 VLXDDLLEA

9

Matches

6

Conservative

ļ. Pred. No.

Mismatches ٥

0;

0;

Local Similarity

Search completed: December 27, 2002, 14:41:38 Job time : 57 secs

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cc has tissue and development of the products system (LNS) and cc has tissue and development-specific expression. The products of the cc invention have nootropic, neuroleptic and antidepressant activity and can be used for gene therapy and antisense inhibition. The method also cd describes a method for producing (1) antisense RNA that is complementary to DNA as above, which can reduce or inhibit synthesis of the protein cc specifically binds to and cleaves transcribed DNA, which reduces or cc inhibits synthesis of the protein coding DNA; (2) a ribozyme, which is complementary to DNA as above, which encodes antisense RNA or a ribozyme; (4) a host cell transformed with a vector as in (3); (5) a protein, cc encoded by DNA as above; (6) a method to produce the protein from the cell or the culture medium; (7) an antibody stargeted against the protein of (5); (8) a diagnostic method to detect disturbed expression of the protein of (5); (8) a diagnostic where the naturally occurring T gene has an cc altered gene structure or sequence; and (11) a method of (8); (10) a conhuman animal as in (10). The DNA, derived from the T gene encodes a T protein (TP) which is involved in development of the central nervous cystem. Antisense sequences, ribozymes and antibodies are useful for cc depression and mental retardation. This sequence represents a fraoment of cc depression and mental retardation. This sequence represents a fraoment of cc depression and mental retardation. This sequence represents a fraoment of comparing the calculating schizophrenia, autism, manic comparing the calculating schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T gene; murine; central nervous system development; CNS; nootropic; neuroleptic; antidepressant; gene therapy; antisense; treatment; schizophrenia; autism; manic depression; mental retardation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding a protein involved in development of the central nervous system (CNS), antisense sequences, ribozymes and antibodies, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE19908423-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel DNA sequence, which encodes a that is involved in development of the central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 12; 86pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of, e.g. schizophrenia and manic depression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-AUG-2000
                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                              depression and mental retardation. This sequence represents a the murine {\mathbb T} protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-580150/55.
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                                                                                         565 AA;
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                         76.3%;
                                            Score 29;
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7.3e+02;
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Result
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Match
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AB1794
T126975
A28180
G87793
AB3794
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  134840
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J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                               type I restriction modification enzyme, subunit M - Methanobacterium thermoautotrophicum
C:Species: Methanobacterium thermoautotrophicum
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Matches
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A;Gene: pepA
C;Superfamily: cytosol aminopeptidase
                                                                                                                                                                                                                                                                                                                                                               leucyl aminopeptidase A [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 23-Mar-2001 C;Accession: G86538
                                                                                                                                 C; Genetics:
                                                                                                                                        A;Cross-references: GB:BA000008; NID:g8978757; PIDN:BAA98593.1; GSPDB:GN00142 A;Experimental source: strain J138
                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-499 <STO>
                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                      A;Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                            R;Shirai, M.; Hirakawa, H.; Kimoto, M.;
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
A; Gene: K04A8.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-174 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published_errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069813; PMID:9851916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: C89075
R;anonymous, The C. elegans:
Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein K04A8.9 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May_2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references:
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C;Superfamily: type I site-specific deoxyribonuclease chain hsdM
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A; Residues: 1-616 <MTH>
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                             Query Match
Best Local
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Conservative
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                 86.8%;
77.8%;
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77.8%;
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                 Pred.
                                        Score 33;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba,
Mismatches
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                 No.
                    51;
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                                      DB 2;
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                                 Length 499;
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Gaps

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leucine aminopeptidase CP0370 [imported] - Chlamydophila pneumoniae (strains CWL029 and N;Alternate names: leucyl aminopeptidase A C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (c;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Accession: G72083; F81583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: F81583
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A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE001623; GB:AE001363; NID:g4376662; PIDN:AAD18529.1; PID:g437666
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
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A;Description: Nucleotide sequence and characterization of glnBA operons of the purple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nitrogen regulatory protein P-II - Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
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C; Superfamily: cytosol aminopeptidase
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                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-112 <ZIN>
A; Cross-references: EMBL: X71659; NID: 9297112; PIDN: CAA50650.1; PID: 9809751
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S33180
A; Accession: S33180
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                                                                                                                                                                       A; Start codon: GTG C; Function:
                                                                                                                                                                                                                                                                  A; Experimental source: strain C; Genetics:
C; Superfamily: regulatory protein P-II
                                                       A; Note: P-II indirectly controls the transcription of the GS gene (glnA) by preventing
                                                                                                               to form P-II-UMP; P-II-UMP allows the deadenylation of glutamine synthetase, thus active
                                                                                                                                           A; Description: important for the control of glutamine synthase; in nitrogen-limiting cor
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                               ted,
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                                  these events are reversed
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Pred. No.
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SPAC1486.03c [imported] - fission yeast (Schizosaccharomyces pomC;Species: Schizosaccharomyces pombe C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                        Science 294, 849-852, 2001

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; We A; Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Accession: AB1663
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A;Experimental source: strain 972h(-); cosmid c1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-797 <MCD>
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A; Accession: T50072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T50072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sugar ABC transporter, permease protein homolog lin1843 [imported] - Listeria innocua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB1663
                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-276 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: AB1663
QΥ
                                                                                                                                 C; Superfamily: maltose transport protein malG
                                                                                                                                                             A; Gene: lin1843
                                                                                                                                                                                                   A; Experimental source: strain Clip11262
                                                                                                                                                                                                                        A;Cross-references: GB:AL592022; PIDN:CAC97074.1; PID:g16414345; GSPDB:GN00178
                                                                                                                                                                                                                                                                                            A; Status: preliminary
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nes 7; Conserv
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                                               Local Similarity
nes 6; Conserv
  2 LXDDLLEA 9
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Pred. No.
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Pred. No. 1.4e+02;
                                                                      Score 31;
Pred. No.
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                                                                    DB . 68;
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                                                                                                Length 276;
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165 ISDDLLEA 172

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R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
                                                                                          C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C:Accession: C81175
                                                                                                                                        UTP-glucose-1-phosphate uridylyltransferase NMB0638 [imported] - Neisseria meningitidis C:Species: Neisseria meningitidis
                     Science 287, 1809-1815,
                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Parkhill, J.; Achtman, M; Holroyd, S.; Jagels, K.; Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AL162754; GB:AL157959; NID:97379424; PIDN:CAB84129.1; PID:9737956
A;Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D81930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-IA; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1291
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C:Species: Listeria monocytogenes
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Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fslhi,
                                                                                                                                                                                                                                                                                         130 ILADDLIDA 138
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                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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75.0%;
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Query Match
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A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A; Map position: 1
                      A; Gene: C27A12.7
                                                                A; Cross-references:
                                                                                        A; Molecule type: DNA
A; Residues: 1-497 <S'
                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                     R; anonymous, The C. elegans s
Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                            C; Accession:
                                                                                                                                                                                                                                                                                                                              C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                 protein C27A12.7 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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A; Residues: 1-397 < MOR>
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C:Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 07-Aug-1998
C:Accession: A28180
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J. Bacteriol. 170, 3125-3130, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) large chain - Met
N;Alternate names: carbamoyl-phosphate synthetase (glutamine-hydrolyzing), ammonia
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A; Residues: 1-289 < TET>
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                                            GB:chr_I; PIDN:AAB93644.1; PID:g2105479; GSPDB:GN00019; CESP:C27A
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66.7%;
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Score

31;

DB 2;

Length 497;

Indels

0;

Gaps

0;

Wood, G.E.; Chen,

Y . ;

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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Stratus. Section 183794
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B83794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T13647
C;Accession: T13647
R;Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
R;Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
R;Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
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R;Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
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R;Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
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R;Ferraz, C.; Vidal, S.; Brun, C.; Brun, C.; Bucheton, A.; Demaille, J.G.
R;Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
R;Ferraz, C.; Vidal, S.; Brun, C.; Brun, C.; Bucheton, A.; Demaille, J.G.
R;Ferraz, C.; Vidal, S.; Brun, C.; Brun,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein 95B7.8 - fruit fly (Drosophila melanogaster) C:Species: Drosophila melanogaster C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change I C:Accession: T13647 R:Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille. J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA A;Residues: 1-750 <STO> A;Residues: 1-750 <STO> A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB04873.1; GSPDB:GN00 A;Experimental source: strain C-125
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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hypothetical protein Y47H9C.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26975
R;Harris, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: FlyBase:FBgn0000376
A;Introns: 94/3; 833/3; 937/3
A;Note: EG:95B7 8
C;Superfamily: fruit fly hypothetical p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AL021728; PIDN:CAA16820.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1042 <FER>
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                                                                                                                                                                               RESULT 16
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Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
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Best Local Similarity
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nes 7; Conserv
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Pred. No.
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3e+02;
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2.1e+02;
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A; Residues: 1-72 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 11-Jan-2002 #sequence_revision 11-Jan-C;Accession: AB3246
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вb
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                                                                                                                                                                                                                                                                                                                                                                                serine/threonine protein kinase-like protein · Arabidopsis thaliana N;Alternate names: protein T17J13.180 C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl, Katp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001

A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transposase tnp [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plasmid {\tt T}
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                                                               A; Experimental source: cultivar Columbia;
                                                                                                                        A; Molecule type: DNA
A; Residues: 1-361 <RIE>
                                                                                                                                                                                                          A; Reference number: Z24482
A; Accession: T48014
                                                                                                                                                                                                                                                                       submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                  R; Rieger,
                                                                                                                                                                                                                                                                                                                             C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C;Accession: T48014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AE008690; PIDN: AAL46384.1;
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A;Accession: AB3246
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                                          C; Genetics:
                                                                                                A; Cross-references: EMBL: AL138651
                                                                                                                                                                                  A; Status: preliminary
            A;Map
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            position: 3
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6; Conserva
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75.0%;
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75.0%;
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Pred. No. 1.2e+02,
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Mewes, H.W.; Lemcke,

K.; Maye

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submitted to GenBank, June 2000, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; A; Matuhors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiteri, D.A Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                           R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
               A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain 9a5c
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross: references: GB:AE003979; GB:AE003849; NID:g9106520; PIDN:AAF84305.1; GSPDB:GN00:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:20365717; PMID:10910347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: PAB2149
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-623 <KAW>
A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49220.1; PID:g545773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues:
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A;Description: Pyrococcus abyssi genome sequence:
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C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text change 20-Jun-2000
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A;Note: T17713.180
C;Superfamily: kinase-related transforming protein; protein kinase homology
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:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
:Accession: E75221
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Pred. No. 2.7e+02.

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Pred. No. 1.5e+02;
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C; Species: Nostoc sp
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A;Cross-references: GB:U18466; NID:g780375; PIDN:AAA65302.1; PID:g780442 C;Superfamily: African swine fever virus probable helicase II B962L C;Seywords: ATP; nucleotide binding; P-loop F:56-63/Region: nucleotide-binding motif A (P-loop) F:163-168/Region: nucleotide-binding motif B F:167-170/Region: DEAH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Yanez, R.J.; Rodriguez, J.M.; Boursnell, M.; Rodriguez, J.F.; Vinuela, E. Gene 134, 161-174, 1993
A:Title: Two putative African swine fever virus helicases similar to yeast 'DEAH' pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       helicase II-like protein, B962L - African swine fever virus
C:Species: African swine fever virus, ASFV
C:Date: 10-Se__1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
hypothetical protein all1696 [imported] - Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-962 < YAN>
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C;Superfamily: SH3 homology
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R;Wong, W.T.; Carlomagno, F.; Druck, T.; Barletta, C.; Croce, C.M.; Huebner, K.; Krau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
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                                                                                                         584 LLADDLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                552 VLKDDILE 559
                                                                                                                                                                                                            Local Similarity
                                                                                                                                                  1 VLXDDLLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 VLSDDLLQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VLXDDLLE 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .-822 <RES>
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                           591
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                                                                                                                                                                                                            78.9%;
75.0%;
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75.0%;
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75.0%;
                                                                                                                                                                                                        Score 30; DB 1;
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 2;
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB 2;
Pred. No. 3e+02;
                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                            Length 962;
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(strain PCC
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A;Status: PICIANA
A;Nolecule type: DNA
A;Residues: 1-1999 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB78062.1; PID:g17135516; GSPDB:GN00179
A;Cross-references: GB:BA000019; PIDN:BAB78062.1; PID:g17135516; GSPDB:GN00179
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DNA Res. 8, 205-213, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: acetate-CoA ligase homology; acyl carrier protein homology C;Keywords: carrier protein; phosphopantetheine; phosphoprotein F;68-566/Domain: acetate-CoA ligase homology <ACL>F;582-649/Domain: acyl carrier protein homology <ACP1>F;1620-2062/Domain: acetate-CoA ligase homology <ACP1>F;1620-2062/Domain: ac
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C;Superf
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A;Accession: T14165
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F;4198-4620/Domain: acetate-CoA ligase homology <ACL3>
F;4637-4705/Domain: acyl carrier protein homology <ACP4>
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                         hypothetical protein NMA0574 [imported] - Neisseria meningitidis (strain 22491 serogrouf C;Species: Neisseria meningitidis C;C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: C81976 C;Accession: C81976 R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, M.A.; Rajandream, M.; James, K.D.; Bentley, S.D.; Morel R;Parkhill, M.; Disternation R;Parkhil
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A; Residues: 1-4976 < YUS>
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502-506,
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Pred. No. 9.9e+02;
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A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491 A;Reference number: A81775; MUTD:20222556; PMID:10761919 A;Accession: C81976
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A; Residues: 1-78 < PAR>
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A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein AGR_C_3387 [imported] - Agrobacterium tumefaciens (strain C58, C C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
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                                                                                                                                                                                                                                                                                              R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, N.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Goretter, P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE007869; PIDN:AAK87614.1; PID:g15156960; GSPDB:GN00169
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A; Residues: 1-101 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Atu1847 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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                                                                                                                                                                                                  A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; PMID:11743193 A;Accession: AE2803
                                                   C; Genetics:
                                                                      A; Experimental source: strain C58
                                                                                              A;Cross-references: GB:AE008688; PIDN:AAL42843.1; PID:g17740292; GSPDB:GN00186
                                                                                                                         A; Molecule type: DNA
A; Residues: 1-101 <KUR>
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A; Map position: circular chromosome
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ce: serogroup A, strain Z2491
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85.7%;
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A;Cross-references: GB:AE000165; GB:U00096; NID:g1786808; PIDN:AAC73698.1; PID:g1786813 A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                        A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: C64793
                                                                                                                                                                                                                                                                                                 A:Cross-references: GB:M24143; NID:g341118; PIDN:AAA76837.1; PID:g522184 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
                                                A; Gene:
                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-137 <BLAT>
                                                                                                                                                                                  A; Status: nucleic acid sequence not shown; translation not shown
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A; Residues: 1-137 <NAH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: C91903
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A; Residues: 1-137 <LIU>
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C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 01-Mar-2002
C;Accession: B91904; C91903; C64793; C32046; D32047
R;Liu, J; Duncan, K; Walsh, C.T.
J. Bacteriol. 171, 791-798, 1989
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C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv3363c
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A; Residues: 1-119 <SAU>
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submitted to the EMBL Data Library, April 1999
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C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C:Accession: T35859
R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Ra
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A; Accession: T35859
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RESULT 32
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C; Superfamily: Escherichia coli ybdB protein
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                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-137 <STO>
                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                  A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85558
                                                                                                                                                                                                                                                                                                                                                                                                         R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J. iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: H85558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein ybdB [imported] - Escherichia coli (strain 0157:H7, substrain C:Species: Escherichia coli
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A; Residues: 1-137 <HAY>
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A;Accession: D90708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Hayashi,
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C:Date: 18 Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: D90708
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31 LGDDVLEA 38
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                                                                                                           Local Similarity
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S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: A10575
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A;Gene: STY0643
C;Superfamily: Escherichia coli ybdB protein
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R;Hatakeyama, T.; Kaufmann, F.; Schroeter, B.; Hatakeyama, T.
Eur. J. Biochem. 185, 685-693, 1989
A;Title: Primary structures of five ribosomal proteins from the archaebacterium Halobact A;Reference number: S06844; MUID:90076190; PMID:2591382
A;Accession: S06845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ribosomal protein L30 [validated] - Haloarcula marismortui N;Alternate names: ribosomal protein HL16; ribosomal protein HL20 C;Species: Haloarcula marismortui C;Date: 31-Mar-1991 *sequence_revision 31-Dec-1992 *text_change 31-Mar-2000 C;Accession: S1643; S06845; B28926; T46808 R;Scholzen, T.; Arndt, E. wol. Gen. Genet. 228, 70-80, 1991
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A; Residues: 1-137 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Walsh, M.J.; McDougall, J.; Wittmann-Liebold, B.
Biochemistry 27, 6867-6876, 1988
A;Title: Extended N-terminal sequencing of proteins of archaebacterial ribosomes blotted A;Reference number: A28926; MUID:89062418; PMID:3196689
A;Accession: B28926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Organization and nucleotide sequence of ten ribosomal A;Reference number: S16535; MUID:91360093; PMID:1832208 A;Accession: S16543
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A; Residues: 1-154 <SCH>
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A; Residues: 1-82, 'L', 84-147, 149-154 <HAT>
A; Note: the source is designated as Halobacterium marismortui
A; Note: the source is designated as Halobacterium marismortui
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                                                                                                                                                                                                A;Gene: HmaL30
C;Superfamily: rat ribosomal protein L7
C;Keywords: protein biosynthesis; ribosome
C;Keywords: protein biosynthesis; ribosome
F;1-154/Product: ribosomal protein L30 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                     \ensuremath{\mathsf{A}}\xspace ; Note: the protein is designated as ribosomal protein C; Genetics:
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submitted to the EMBL Data Library, July 1996 A; Reference number: Z19244 A; Accession: T20267
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 28-Jul-2000
C;Accession: D72293
C;Accession: D72293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-156 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 5
                   A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 *sequence_revision 14-Dec-2001 *text_change 30-Jun-2002 C;Accession: AI2271
                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: TM1127 C; Superfamily: Thermotoga maritima hypothetical protein TM1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE001770; GB:AE000512; NID:g4981658; PIDN:AAD36203.1; PID:g498
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 399,
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
                                                                                        C; Species: Nostoc sp.
                                                                                                           transcription regulator all3728 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                             RESULT 36
                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: D72293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 DDLLEA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 DDLLEA 9
                                                                                                                                                                                                                             58 LADDLLKA 65
                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                     2 LXDDLLEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evidence for lateral gene transfer between Archaea and Bacteria from genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone C56A3
                                                                                                                                                                                                                                                                                                                                          76.3%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                             Score 29;
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                                                                                                                                                                                                                                                                                                                                             1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                            strain PCC 7120
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S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

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A:Gene: yhhw
C:Superfamily: conserved hypothetical protein sll1773
                                                                                                 C; Genetics:
                                                                                                                  A; Experimental source: strain K-12, substrain MG1655
                                                                                                                               A;Cross-references: GB:AE000420; GB:U00096; NID:g1789840; PIDN:AAC76464.1; PID:g1789847
                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-231 <BLAT>
                                                                                                                                                                                                                                   C;Accession: B65140

R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Tittle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: B65140
                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical 26.3 kD protein in gntR-ggt intergenic region - Escherichia coli (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
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A; Residues: 1-207 <STO>
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A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adman, S.; Yuan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable oxidoreductase PA0853 [imported] - Pseudomonas aeruginosa (strain PA01)
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A:Experimental source: strain PCC 7120
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A;Accession: AI2271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA A; Residues: 1-192 < KUR>
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DNA Res. 8, 205-213, 2001
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les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DDLLEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VLXDDLLEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li
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77.8%;
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100.0%; Pr
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
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1.3e+02;
1.3e+02;
1.3e+02;
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hypothetical protein yibb [imported] - Lactococcus lactis subsp. C; Species: Lactococcus lactis subsp. lactis
                                                                                                                                                         В
                                                             D86725
                                                                                RESULT 41
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A:Gene: yhhW
C;Superfamily: conserved hypothetical protein sll1773
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                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-231 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                           R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J. iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                         A; Experimental source: strain O157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: H86010
                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: H86010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein yhhw [imported] - Escherichia coli (strain O157:H7, substrain ED
C;Species: Escherichia coli
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H91164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-231 <HAY>
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A;Accession: H91164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: H91164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                           Matches
                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Escherichia coli
Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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Matches 5; Conserv
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Best Local Similarity
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42 VINDDVIEA 50
                                                                                      Local Similarity
mes 5; Conserv
                                            1 VLXDDLLEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VLXDDLLEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECs4288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.
                                                                                      Conservative
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                                                                                                         76.3%;
55.6%;
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55.6%;
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55.6%;
                                                                                 3; Mismatches
                                                                                                                              Score 29;
                                                                                                         Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 2;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .5e+02;
                                                                                                                         Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 231;
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yokoyama, K.; Han,
Shinagawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.J.; May
                                                                             0,
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lactis (strain IL140

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C;Genet:
A;Gene:
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Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis sq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: D86725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: D86725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: AE005176; PID: 912723725; PIDN: AAK04902.1; GSPDB: GN00146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-244 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytochrome-c oxidase (EC 1.9.3.1) chain II - yeast (Candida glabrata) mitochondrion C;Species: mitochondrion Candida glabrata G;Date: 07-May:1995 #sequence_revision 14-Jul-1995 #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The structure of the small mitochondrial DNA of Kluyveromyces thermotolerans is A;Reference number: $45322; MUID:94365843; PMID:8083884
A;Accession: $45438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Genome: mitochondrion A;Genetic code: SGC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X69430; NID:g509746; PIDN:CAA49205.1; PID:g728536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-251 <CLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: COXII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: translation not shown
                                                                                                                                                 sensory transduction regulatory protein - Methanobacterium thermoautotrophicum (strain c;Species: Methanobacterium thermoautotrophicum c;Date: 05-Dec:1997 #sequence_revision 05-Dec:1997 #text_change 22-Oct-1999 C;Accession: D69158 C;Accession: D69158 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredde, T.:
                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A;Reference number: A69000; MUID:98037514; PMID:9371463 A;Accession: D69158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: cytochrome-c oxidase chain II; cytochrome-c oxidase chain II homology; Keywords: copper; electron transfer; heme; membrane-associated complex; mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;186,221,225,232/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted;221,225,225,229/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted;223/Binding site: magnesium (Glu) (shared with chain 1) #status predicted;223/Binding site: magnesium (Glu) (shared with chain 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-239/Domain: cytochrome-c oxidase chain II homology <CO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keywords: copper; electron transfer;
                                                                    ;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                             147 VIPDDLLE 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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A;Cross-references: GB:AE000829; GB:AE000666; NID:g2621512; PIDN:AAB84953.1; PID:g262
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-277 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;4-\widehat{1}14/\text{Domain:} response regulator homology <RRH> F;53/\text{Binding site:} phosphate (Asp) (covalent) **status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: response regulator homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: MTH447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor - yeast (Kluyv C;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica C;Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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A; Residues: 1-292 <GBE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: $72323; MUID:96304292; PMID:8660461
A; Accession: $72323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Isolation and molecular analysis of the gene for cytochrome c1 from Kluyvero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S72323
R;Gbelska, Y.; Horva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: the source is designated as Kluyveromyces lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain JBD100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: x95899; NID: 91209427; PIDN: CAA65144 1; PID: 91209428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: cytochrome c1 heme protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:47-292/Product: cytochrome c1 #status predicted <MAT> F:55-281/Domain: cytochrome c1 heme protein homology <C1H>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: chromoprotein; electron transfer; heme; iron; membrane-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;90,210/Binding site: heme iron (His, Met)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;86,89/Binding site: heme (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;254-271/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1-46/Domain: transit peptide (mitochondrion) #status predicted <TNP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Genome: nuclear
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                  A; Reference number: S44620
A; Accession: S44847
                                                                                                                                                  C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
                                                                                                                                                                     C; Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                             A; Description: Sequence of the C. elegans cosmid K06H7
                                                                                    submitted to the EMBL Data Library, May 1993
                                                                                                          R; Favello,
                                                                                                                                 C; Accession:
                                                                                                                                                                                               K06H7.7 protein - Caenorhabditis elegans
                                                                                                                                                                                                                                              RESULT 45
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                              213 VLFDDLVE 220
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les 6; Conser
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                                                                                                              A.D.
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0, 145-150, 1996
                                                                                                                                    S44847
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                                                                                                                                                                                                                                                                                                                                                                                                                             76.3%;
75.0%;
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    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytochrome c1 heme protein homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (axial ligands) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                    1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                             A;Gene: msbB
                                                                                                                                                                       A;Cross-references: GB:AE005174; NID:g12515911; PIDN:AAG56845.1; GSPDB:GN00145; UWGP:229
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-323 <STO>
                                                                                                                                                                                                                                                                                  A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: A85798
                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                         C;Accession: A85798

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         suppressor of htrB, heat shock protein [imported] - Escherichia coli (strain 0157:H7,
C; Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 47
A85798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: ECs2565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:BA000007; PIDN:BAB35988.1; PID:g13362033; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-323 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E90949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Hayashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heat shock protein MsbB [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 05
C:Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 56/1; 116/1; 142/2; 181/3; 281/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:L15314; NID:g289690; PID:g289697 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA **Posidues: 1-322 <FAV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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267 DDLLEA 272
                                                                                               Local Similarity
                                        4 DDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 DDLLEA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 DDLLEA 9
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                                                                            Conservative
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                                                               76....
100.08; F1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.3%; Score 29; DB 2; 100.0%; Pred. No. 2.1e+(
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85.7%;
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Pred. No. 2.1e+02;
                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                 2.1e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1e+02
                                                                                                      Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 323;
                                                               Indels
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                                                         Gaps
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; pMID:11759840
A; Molecule type: DNA
                                                                                                                                                                                                                               A;Note: Nostoc sp. strain PCC 7120 is a Synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AC2367
                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                         glucose-1-phosphate thymidylyltransferase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: transfers myristate or laurate, activated on ACP, to (Kdo)2-(lauroy1)-A;Pathway: lipopolysaccharide core biosynthesis
A;Pathway: lipopolysaccharide core biosynthesis
A;Note: decanoy1, palmitoy1, palmitoleoy1 and (R)-3-hydroxymyristoy1-ACP are poor acy
C;Keywords: acyltransferase; lipopolysaccharide core biosynthesis; transmembrane prot
F;23-43/Domain: transmembrane #status predicted <TMI>
F;85-105/Domain: transmembrane #status predicted <TMI>
F;85-105/Domain: transmembrane #status predicted <TMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE000279; GB:U00096; NID:g1788154; PIDN:AAC74925.1; PID:g17881A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: msbB; mlt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: G64947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M87660; NID:g146876; PIDN:AAA96706.1; PID:g146877
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
-A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
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J. Bacteriol. 174, 6394-6403, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Title: Isolation and characterization of the Escherichia coli msbB gene, a multicop A;Reference number: A42608; MUID:92121107; PMID:1732206
A:Accession: A42608
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A; Residues: 1-323 <KAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Karow, M.; Georgopoulos, C.
J. Bacteriol. 174, 702-710, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 DDLLEA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 DDLLEA 9
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100.0%; Pi
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100.0%; Pred. No.
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probable NADH2 dehydrogenase (EC 1.6.99.3) yjlD - Bacillus subtilis
C:Species: Bacillus subtilis
C:Species: Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C;Date: 10-Sep-1999 #text_chang
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A;Cross-references: GB:BA000019; PIDN:BAB76190.1; PID:g17133627; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4491
C;Superfamily: mannose-1-phosphate guanylyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: electron transfer; FAD; flavoprotein; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13086.1; PID:g2633583 A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-392 <KUN>
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Search completed: December 27, 2002, 14:42:30 Job time : 46~\text{secs}
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Best Local
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nes 6; Conserv
                                                                                                                                                                  205 VLPDDLIE 212
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                              76.3%; Score 29; DB 1; 75.0%; Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 392;
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23 60.5 194 I Y615_PYRAB 23 60.5 195 I GSPJ_ECOLI 23 60.5 199 I RTN4_MOUSE 23 60.5 202 I YF56_MYCTU 23 60.5 204 I QC3_BACSU 23 60.5 204 I VC05_VACCC 23 60.5 204 I VC05_VACCC	973 23 60.5 190 1 APT_TREPA 974 23 60.5 190 1 PTH_STAAM 974 23 60.5 192 1 DEF_THETH 975 23 60.5 192 1 DEF_THETH	970 23 60.5 185 1 YCUC_ECULT 971 23 60.5 186 1 CPEZ_SYMPY 072 23 60.5 187 1 YB35_PYRAB	968 23 60.5 184 1 YPS2_SYNP2 969 23 60.5 185 1 APT_CAESL	966 23 60.5 181 1 Y573_RICPR	964 23 60.5 181 1 Y179_THEAC Q9h1p8	962 23 60.5 179 1 FYRY BACCL 963 23 60.5 179 1 FYRY BACCL 963 27 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	961 23 60.5 177 1 RS13_HALMA	959 23 60.5 175 1 PYRE_HALN1	957 23 60.5 1/1 1 AFT_STAAM 032418	956 23 60.5 170 1 APT_BACSU 034443	954 23 60.5 166 1 YVAE_VACCC 058219	952 23 60.5 165 1 VIJIENT P55670 P20514	950 23 60.5 157 1 BFRB_NEWA P56999 951 23 60.5 157 1 BFRB_NEWA P16792	949 23 60.5 156 1 BFR AZOVI P77914 949 23 60.5 157 1 BFRB NEIGO P77914	947 23 60.5 154 1 GP41_BPSP1 048397 048 23 60.5 154 1 SM20_SCHMA P15845	23 60.5 151 1 YPH7 CHRVI P45371 23 60.5 153 1 Y553 METJA Q57973	23 60.5 148 1 LYC_SAISC P79294 23 60.5 149 1 UREE LACFE Q9x525	941 23 60.5 148 1 LYC2_RAT 005820	23 60.5 141 1 LYCN_BOVIN PROTES 23 60.5 147 1 YDEF_SCHPO Q10446	23 60.5 138 1 RBFA AGRT5 Q8u)52 23 60.5 140 1 VPC BPMU P06022	23 60.5 134 1 YBGC_ECOLI P08999 23 60.5 137 1 LYC_BOMMO P48816	23 60.5 132 1 Y16K_SSV1 P18818	23 60.5 130 1 LYCK_SHEEP P16973 23 60.5 130 1 LYC_RABIT P201018	23 60.5 127 1 UCK/_KLULA P81709 23 60.5 130 1 LYC2_CANFA P80100	23 60.5 127 1 RL7A_SULSO P55858	23 60:5 125 1 FABL_ANOPU Q90239 23 60:5 125 1 V568 METTA Q57988	23 60.5 120 1 PAND_RALSO Q8XVUO 23 60.5 124 1 CY51 SCHPO 094391	23 60.5 119 1 YRF4_SHIFL P37790	23 60.5 113 1 SUII_MOUSE P48024	23 60.5 113 1 SU13_HUMAN P41567	23 60.5 112 1 FEK_FSEAE Q9ung9	23 60.5 109 1 VMII_IACAO P26147	23 60.5 106 1 WOLFFENT P10278 23 60.5 106 1 YIZK_BP94 P10278 25 60.5 107 1 RIAI CHLRE P29763	23 60.5 9/ 1 FEATLARING 27255 23 60.5 99 1 YB87_METTH 027255 25 60.5 100 1 WILL M DHYTN 037598
23 60.5 194 1 23 60.5 199 1 23 60.5 202 1 23 60.5 204 1 23 60.5 204 1 23 60.5 204 1 23 60.5 204 1	973 23 60.5 190 1 APT_TREPA 084001 974 23 60.5 190 1 PTH_STAAM 099wa1 974 23 60.5 190 1 PTH_STAAM P43522 975 23 60.5 192 1 DEF_THETH 09007074	970 23 60.5 185 1 YCUC_ECULI 971 23 60.5 186 1 CPEZ_SYNPY Q02175 972 23 60.5 187 1 YB25_PYRAB Q9uxz1	968 23 60.5 184 1 YPS2_SYNP2 969 23 60.5 185 1 APT_CAESL	966 23 60.5 181 1 Y573_RICPR 090054 967 23 60.5 182 1 PAAD_ARCFU 021526	964 23 60.5 181 1 Y179_THEAC Q9h1p8	962 23 60.5 179 1 PARK_BAUCH P44722 963 23 60.5 171 TABLE BASEN P39765	960 23 60.5 177 1 RS13_HALMA Q00861 ha.	959 23 60.5 175 1 PYRE_HALN1	957 23 60.5 1/1 1 AFT_STAAM 032418 stap	956 23 60.5 170 1 APT_BACSU 034443	954 23 60.5 166 1 YVAE_VACCC (2001) Net	952 23 60.5 15/1 VIJI-INVIN P55670 rhizob	950 23 60.5 157 1 BFRB_NEIMA P16792 hume	949 23 60.5 156 1 BFR AZOVI P77914 949 23 60.5 157 1 BFRB NEIGO P77914	947 23 60.5 154 1 GP41 BPSP1 048 23 60.5 154 1 SM20_SCHMA	23 60.5 151 1 YPH7 CHRVI P45371 23 60.5 153 1 Y553 METJA Q57973	23 60.5 148 1 LYC_SAISC P79294 S	941 23 60.5 148 1 LYC2_RAT 005820	23 60.5 141 1 LYCN_BOVIN PROTES 23 60.5 147 1 YDEF_SCHPO Q10446	23 60.5 138 1 RBFA_AGRT5 Q8uj52 agro	23 60.5 134 1 YBGC_ECOLI P08999 23 60.5 137 1 LYC_BOMMO P48816	23 60.5 132 1 Y16K_SSV1 P18818	23 60.5 130 1 LYCK_SHEEP P16973 23 60.5 130 1 LYC_RABIT P201018	23 60.5 127 1 UCK/_KLULA P81709 23 60.5 130 1 LYC2_CANFA P80100	23 60.5 127 1 RLTA_SULSO P55858 sul.	23 60.5 125 1 FABL_ANOPU 23 60.5 125 1 V568 METTA	23 60.5 120 1 PAND_RALSO	23 60.5 119 1 YRF4_SHIFL P37790 sh	23 60.5 113 1 SUIT MOUSE	23 60.5 113 1 SU13_HUMAN P41567 homo se	23 60.5 112 I FER_FSEAE 29ung9 homo	23 60.5 109 1 VMT1_IACAO	23 60.5 100 1 NOLIT FILE PLAN P10278 23 60.5 106 1 Y12K_BPP4 P10278 23 60.5 107 1 RIAI CHLRE P29763	23 60.5 9/ 1 FEATLARING 27255 23 60.5 99 1 YB87_METTH 027255 25 60.5 100 1 WILL M DHYTN 037598

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Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.",
                                                                                                                                                                                                                                                       Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBcy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
                                                                                                             Nucleic Acids Res.
                                                                                                                                                                      MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                        Nucleic Acids Res. 28:1397-1406(2000).
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                                                                                                                                                                                                                                            "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                          MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q928F8; Q9JQJ2;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable cytosol aminopeptidase (EC 3.4.11.1)
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99206606; PubMed=10192388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LAP) (Leucyl aminopeptidase). PEPA OR CPN0385 OR CP0370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=83558;
                  CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
Xbb-, in which Xaa is preferably Leu, but may be other amino acids
including Pro although not Arg or Lys, and Xbb may be Pro.
         COFACTOR: MANGANESE (BY SIMILARITY)
                                                                               FUNCTION: PRESUMABLY INVOLVED IN THE PROCESSING AND REGULAR TURNOVER OF INTRACELLULAR PROTEINS. CATALYZES THE REMOVAL O
                                                               SIMILARITY)
                                                                 TURNOVER OF INTRACELLULAR PROTEINS. CATALYZES THE REMOVAL CUNSUBSTITUTED N-TERMINAL AMINO ACIDS FROM VARIOUS PEPTIDES
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                                                                                                          28:2311-2314(2000)
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DEOC_BACSU
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                or Lys, and Xbb may
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Q9k0m6
P54988
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P26998
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GLNB_RHOSH
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Best Local
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P43519;
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ACT_SITE
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RESULT 1

CHLPN

AMPA_CHLPN

986 987 988 989 990 991 992 993 994 995 995 996 999

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Zinchenko V.V., Churin Y., Shestopalov V.I., Shestakov S.V.;
"Nucleotide sequence and characterization of the Rhodobacter sphaeroides glnb and glna genes.";
Microbiology 140:243-2151(1994).
-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA, WHEN P-II IS URIDYLYLATED TO P-II-UMP, THESE DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, THESE DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE ENZYME.
-!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P(II) PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
                                                                                                                                                                                                                                                                                                       MEDLINE=95005468; Pubmed=7921264;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nitrogen regulatory protein P-II (PII signal transducing protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by anoforcement is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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METAL 263 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001623; AAD18529.1; -. EMBL; AE002199; AAF38219.1; -. EMBL; AP002546; BA98593.1; -. HSSP; P00727; 1BPN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteobacteria; alpha subdivision; Rhodobacter group;
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499
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77.8%;
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MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B0F281B1DF4B9EC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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SO PETERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P13258;
(01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthese large chain (EC 6.3.5.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proDom; PD001194; PII_glnB; 1.
proSITE; PS00496; PII_GLNB_CTER; 1.
proSITE; PS00638; PII_GLNB_CTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X71659; CAA50650.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; Nitrogen fixation BINDING 51 51 UMP (BY SIMILA)
                                                                                                                                                                                                                                                                                                    Methanosarcina barkeri MS and Methanococcus vannielii.";

J. Bacteriol. 170:3125-3130(1988).

-i- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = phosphate + L-glutamate + carbamoyl phosphate.

-i- COFACTOR: Binds three manganese ions (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARB_METBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00340; PIIGLNB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002332; PII_GlnB_UMP.
InterPro; IPR002187; PII_glnB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P38504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanosarcina barkeri.
                                                                                                                                                                                                                                                                                                                                                                                               "Conservation of structure in the human gene encoding argininosuccinate synthetase and the argG genes of the archaebacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88257029; PubMed=3133361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MS / DSM 800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
                                                                                                                                                                                                                                                                                                                                                                                                                               Morris C.J., Reeve J.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanosarcinaceae; Methanosarcina.
                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                           the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                       -!- PATHWAY: Arginine biosynthesis
                    EMBL; M21314; AAA72676.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                              PATHWAY: Pyrimidine biosynthesis; first step.
SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate.
SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00543; P-II; 1
                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6;
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                                                                                                       non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                          this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B278486AC9EB17D3 CRC64;
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                                                                                                             as its content
                                                                                              Usage
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CARB_METMA
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pfam; PF02786; CPSASE_L_D2; 1.
pROSITE; PS00866; CPSASE_2; 1.
pROSITE; PS00867; CPSASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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InterPro; IPR004362; MGS_like.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                 Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A., Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;

MEDLINE=22120827; PubMed=12125824;

MEDLINE=21120827; PubMed=12125824; Marki R. Schil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Methanococci; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanosarcina mazei (Methanosarcina frisia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARB OR MM0038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARB_METMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphate synthetase ammonia chain).
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                           -!- PATHWAY: Arginine biosynthesis.
-!- PATHWAY: Pyrimidine biosynthesis; first step.
-!- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By
                                                                                                                                                                                                                                                                                                                                                                            "The genome of Methanosarcina mazei: evidence for lateral gene
                                                                                                                                                                                                                                                                                                                                                                                           Fritz H.-J., Gottschalk G:;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2209;
                                                                                      modified and this statement is not removed. entities requires a license agreement (See
                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                   the European Bioinformatics Institute.
                                            EMBL; AE013223; AAM29734.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                               similarity).
SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biosynthesis; Pyrimidine biosynthesis; Ligase; Manganese
                                                                                                                      pean Bioinformatics Institute. There are no restrictions non-profit institutions as long as its content is in
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146
158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253
398
146
158
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                                                                                           license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 398
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                                                                                                              and for commercia.
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PROSITE;

Arginine

biosynthesis; PS00866; CPSASE_1; PS00867; CPSASE_2;

Pyrimidine biosynthesis; Ligase; Repeat;

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Best Local
                                                             InterPro; IPR000050; PID_domain InterPro; IPR001452; SH3,
                                                                                                                                                                                                                          entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                        ProDom;
                                            Pfam; PF00018; SH3;
                                                                                                                                                             HSSP; Q08509;
                                                                                                                                                                                EMBL; U12535; AAA62280.1;
                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncogene 9:3057-3061(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Evolutionary conservation of the EPS8 gene and its mapping to human chromosome 12q23-q24.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wong W.T., Carlomagno F., Druck T., I
Huebner K., Kraus M.H., di Fiore p.p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=94366758; PubMed=8084614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; V. Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Epidermal growth factor receptor kinase substrate EPS8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPS8_HUMAN
Q12929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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DOMAIN 1 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 1 PH DOMAIN. IT IS SPLIT IN TWO PARTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: UPON BINDING TO EGF RECEPTOR ENHANCES EGF-DEPENDENT MITOGENIC SIGNALS. CAN BIND MULTIPLE CELLULAR TARGETS.

TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES ANALYZED, INCLUD: HEART, BRAIN, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY & PANCREAS. EXPRESSED IN ALL EPITHELIAL AND FIBROBLASTIC LINES EXAMINED AND IN SOME, BUT NOT ALL, HEMATOPOIETIC CELLS.

PTM: PHOSPHORYLATED BY SEVERAL RECEPTOR TYROSINE KINASES.
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MANGANESE 1 AND 2 (BY SIMILARITY).
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                                                             Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H. Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                 the European Bioinformatics Institute.
                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                              Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                          Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                   MEDLINE-89123154; PubMed=2521621; Mahlik M.S., Brickman T.J., Ozenberger B.A., McIntosh M.A.; "Nucleotide sequence and transcriptional organization of the Escherichia coli enterobactin biosynthesis cistrons entB an
                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                         STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                            biosynthesis genes: identification of entA and purification of product 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase.";
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01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Hypothetical protein; Complete proteome.

SEQUENCE 137 AA; 14970 MW; C8DF8DE63815F206 CRC64;
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16-OCT-2001
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                                                                                                                                                                                      SEQUENCE OF 1-30.

MEDLINE=89062418; PubMed=3196689;

Walsh M.J., McDougall J., Wittmann-Liebold B.;

"Extended N-terminal sequencing of proteins of ar ribosomes blotted from two-dimensional gels onto poly(vinylidene diffluoride) membrane.";

Biochemistry 27:6867-6876(1988).
                                                                                                                                                                                                                                                                                                                  Hatakeyama T., Kaufmann F., Schroeter B., Hatakeyama T.; "Primary structures of five ribosomal proteins from the archaebacterium Halobacterium marismortui and their structural relationships to eubacterial and eukaryotic ribosomal proteins."; Eur. J. Biochem. 185:685-693(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                            from the region equivalent to the spectinomycin operon archaebacterium Halobacterium marismortui."; nol. Gen. Genet. 228:70-80(1991).
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Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
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Scholzen T., Arndt E.;
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                              A resolution.";
Science 289:905-920(2000).
-!- SIMILARITY: BELONGS TO THE L30P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS). STRAIN=ATCC 43049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Organization and nucleotide sequence of ten ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacteriaceae; Haloarcula.
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MuG-1992 (Rel. 23, Last sequence update)
CCT-2001 (Rel. 40, Last annotation update)
ribosomal protein L30P (Hmal30) (HL20) (HL16).
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                                                                                             Hansen J., Moore P.B., Steitz T.A.; ic structure of the large ribosomal subunit at 2.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00327; Ribosomal_L30; 1.
TIGRFAMS; TIGR01309; L30P_arch; 1.
                                                                                                                                                                                                                                                                                        Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K. Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein yhhw.
YHHW OR Z4807 OR ECS4288.
Escherichia coli O157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P58116;
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000517; Ribosomal_L30.
                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=0157:H7 / F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=0157:H7 / E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                               DNA
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MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of enterohaemorrhagic Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L6-OCT-2001 (Rel.
L5-JUN-2002 (Rel.
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    !- SIMILARITY: BELONGS TO THE PIRIN FAMILY.

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                                                                                                                                                                                                                                                                            8:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148
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MISSING (IN REF. 2).
ED673F036E974C14 CRC64;
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Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision; Enterobacteriaceae;
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                                                         (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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Best Local
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                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                         SEQUENCE
                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                   Complete proteome.
                                                                                                                                                 InterPro;
                                                                                                                                                            EcoGene; EG12943;
                                                                                                                                                                                                                                                                                                                                      Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs "Enrichment of low abundance proteins of Escherichia coli by hydroxyapatite chromatography."; Electrophoresis 20:2181-2195(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99420866;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Science
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01-NOV-1995 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE PIRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mau B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION BY MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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EMBL; AP002565; BAB37711.1;
InterPro; IPR003829; DUF209.
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 42
                                                                   Local Similarity
                           1 VLXDDLLEA 9
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les 5; Conser
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VINDDVIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                  complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
                                                                                                                                   PF02678; DUF209; 1.
                                                                                                                                                                         AE000420; AAC76464.1; -.
                                                                                                                                                                                        U18997; AAA58237.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shao Y.;
                                                                                                                                                IPR003829;
                                                                                                         231 AA;
                                                    Conservative
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32, Last sequence update)
40, Last annotation update)
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                                                                                                        26279 MW;
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                                                                   76.3%;
55.6%;
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55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma subdivision; Enterobacteriaceae;
                                                              Score 29;
Pred. No.
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                                                                                                      62E5B21331686935 CRC64;
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                                                 Mismatches
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                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rode C.K., Mayhew G.F.,
                                                                           Length 231;
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RESULT 11
CY1_KLULA
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                                                                                                                                            Query Match
Best Local
             CY1_KLULA
Q00988;
01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                       Pfam; PF00116; COX2; 1.

Pfam; PF02790; COX2 TM; 1.

PRINTS; PR011165; CYCOXIDASEII.

ProDom; PD000131; Copper_CuA; 1.

PROSITE; PS00078; COX2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                     Electron transport;
                                                                                                                                                                                                                                                Oxidoreductase; Copper; Mitochondrion; Transmembrane;
                                                                                                                                                                                                                                                                                                                 InterPro; IPR001505; Copper_CuA.
InterPro; IPR002429; Cyt_c_ox_2.
                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94365843; PubMed=8083884; Clark-Walker G.D., Weiller G.F.; "The structure of the small mitochondrial DNA of Kluyveromyces thermotolerans is likely to reflect the ancestral gene order in
                                                                                  147 VIPDDLLE 154

    -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

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01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CBS 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candida glabrata (Yeast) (Torulopsis glabrata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fungi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales; mitosporic Saccharomycetales; Candida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COX2_CANGA
                                                                                                                                           Local
                                                                                                        1 VLXDDLLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                Similarity 6; Conserv
                                                                                                                                                                            186
221
225
229
251 AA;
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                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
coxidase polypeptide II (EC 1.9.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copper A
                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                  186
221
225
                                                                                                                                                                                        229
                                                                                                                                                                            28662 MW;
                                                                                                                                                                                                                                   Respiratory chain
                                                                                                                                         76.3%;
75.0%;
                                                                                                                             1; Mismatches
                                                                                                                                                                                      COPPER A
                                                                                                                                                                                                 COPPER A (PROBABLE).
COPPER A (PROBABLE).
COPPER A (PROBABLE).
                                                                                                                                         Score 29;
Pred. No.
                                                                                                                                                                           9F3FC7BC1ED6BEC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                        292
                                                                                                                                                                                      (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 AA
                                                                                                                                                     DB 1;
                       ΑA
                                                                                                                                                   Length 251;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            order in
                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                     commercia
                                                                                                                                                                                                                                                                                                                                                                                                  on
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В
RESULT 12
                                                                                                                                                                                                                                YMX7_CAEEL
                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kluyveromyces lactis.";
Curr. Genet. 30:145-150(1996).

-i- FUNCTION: THIS IS THE HEME-CONTAINING COMPONENT OF THE CYTOCHROME
-i- FUNCTION: THIS IS THE HEME-CONTAINING COMPONENT OF THE CYTOCHROME
B-C1 COMPLEX, WHICH ACCEPTS ELECTRONS FROM RIESKE PROTEIN AND
TRANSFERS ELECTRONS TO CYTOCHROME C IN THE MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytochrome c1, heme protein, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content imodified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steensma H.Y., Subik J.; resolution and molecular analysis of the gene for cytochrome cl from resolution and molecular analysis of the gene for cytochrome cl from resolutions.
                                                                                                                                             01-FEB-1994
01-FEB-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR000345; CytC_heme_bind.
Interpro; IPR002326; Cyt_C1.
Pfam; PF02167; Cytochrome_C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gbelska Y., Horvathova K., van der Aart Q.J.M., Zonneveld B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96304292; PubMed=8660461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prINTS; PR00603; CYTOCHROMEC1.
prOSITE; PS00190; CYTOCHROME_C; 1.
Electron transport; Respiratory chain; Oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X95899; CAA65144.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 37.6 kDa protein K06H7.7 in chromosome III.
                                                                                                                                                                                               YMX7_CAEEL 
P34515;
STRAIN-Bristol N2
                 SEQUENCE FROM N.A.
                                                               Rhabditidae; Peloderinae;
                                                                             Eukaryota; Metazoa;
                                                                                                Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                213 VLFDDLVE 220
                                                                                                                                                                                                                                                                                                                                                                                Loca 1
                                                                                                                                                                                                                                                                                                                               1 VLXDDLLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B. CYTOCHROME C1 AND THE RIESKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESPIRATORY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion; Transit peptide.

Mitochondrion (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                               Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               292 AA;
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                             46
292
86
86
89
1
90
210
31947 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetaceae; Kluyveromyces
                                                                                 Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                76.3%;
75.0%;
                                                                 Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEME
                                                                                                                                                                                                                                                                                                                                                                                                                                IRON (HEME AXIAL LIGAND)
07F909B81B1C1C72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOCHROME C1
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              (HEME AXIAL LIGAND).
(HEME AXIAL LIGAND) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COVALENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COVALENT).
                                                                                                                                                                                                                   322 AA
                                                                                                                                                                                                                                                                                                                                                                                   рв
79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEME PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                 Length 292;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for commercia.
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Query Match
Best Local Similarity
6; Conserva
Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
MSBB_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen i
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1992 (Rel. 21, List sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase
(EC 2.3.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein SEQUENCE 322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WormPep; K06H7.7; CE00258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L15314; AAF99983.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wohldman P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S44847; S44847
                                                                                                                                                                                                                        Karow M., Georgopoulos C.;
"Isolation and characterization of the Escherichia coli msbB gene,
multicopy suppressor of null mutations in the high-temperature
                                                                                                                                                                                                                                                                             STRAIN-K12 / W3110;
MEDLINE=92121107; PubMed=1732206;
                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P24205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSBB_ECOLI
                                               "Murein-metabolizing enzymes from Escherichia coli: existence second lytic transglycosylase.";
J. Bacteriol. 174:6394-6403(1992).
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                   Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                     MSBB OR B1855
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                 J. Bacteriol.
[3]
                                                                                                   MEDLINE=93015688; PubMed=1356966; Engel H., Smink A.J., van Wijngaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 LADDLLE 227
                                                                                                                                                                                                         requirement
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LXDDLLE 8
                                                                                                                                                                                           Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                           gene htrB.";
1, 174:702-710(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                   .J., van Wijngaarden L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37625 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.3%;
                                                                                                                                                                                                                                                                                                                                                                                      gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D3A874DCF2C0176D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 322;
                                                                                                          Keck W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shownkeen R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coulson A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RANGE FOR THE PROPERTY OF THE 
                                                                                                                               Matches
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                              Pfam; PF03279; Lip_A_acyltrans; 1.
Lipopolysaccharide biosynthesis; Transferase; Acyltransferase;
Transmembrane; Inner membrane proteome.
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M87660; AAA96706.1; -. EMBL; AE000279; AAC74925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M77039; AAA24181.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            follows laurate incorporation by HtrB.";

J. Biol. Chem. 272:10353-10360(1997).

-i- FUNCTION: TRANSFERS MYRISTATE OR LAURATE, ACTIVATED ON ACP, TO THE LIPID IVA MOIETY OF (KDO)2-(LAUROYL)-LIPID IVA. DECANOYL, PALMITOLEOYL, AND (R)-3-HYDROXYMYRISTOYL-ACP ARE POOR ACYL DONORS. FUNCTIONS OPTIMALLY AFTER LAURATE INCORPORATION BY HTRB HAS TAKEN PLACE. ACYLATES (KDO)2-(LAUROYL)-LIPID IVA ABOUT 100 TIMES FASTER THAN (KDO)2-LIPID IVA. DISPLAYS A PREFERENCE FOR MYRISTOYL-ACP OVER LAUROYL-ACP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EcoGene; EG10614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97251358; PubMed-9097040;
Itch T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
Salto N., Sampei G., Seki Y., Styasundaram S., Tagami H.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
"A 460-kb DNA sequence of the Escherichia coli K-12 genome
Corresponding to the 40.1-50.0 min region on the linkage map.",
DNA Res. 3:379-392(1996).
267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clementz T., Zhou Z., Raetz C.R.H.;
"Function of the Escherichia coli msbB gene, a multicopy suppressor of htrB knockouts, in the acylation of lipid A. Acylation by MsbB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97256743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453\cdot1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mau B.,
                                                            4 DDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Lipopolysaccharide core biosynthesis.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
SIMILARITY: BELONGS TO THE HTRB/MSBB FAMILY.
DDLLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE MEMBRANE-BOUND LYTIC MUREIN TRANSCLYCOSYLASE (MLT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A42608; A42608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D90828; BAA15663.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR004960; LipA_acyltrans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND CHARACTERIZATION
272
                                                                                                                                                                                                                                                 323 AA;
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        msbB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=9099672;
                                                                                                                                                                                                                                                 37410 MW;
                                                                                                                                                   100.0%;
                                                                                                                                                                                 76.3%;
                                                                                                                                               Score 29; 
; Pred. No.
                                                                                                                 0;
                                                                                                                                                                                                                                                                               POTENTIAL
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                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                       94DAF38A757D20CD CRC64;
                                                                                                                 Mismatches
                                                                                                                                               88;
                                                                                                                                                                          1;
                                                                                                           0;
                                                                                                                                                                          Length 323;
                                                                                                           Indels
                                                                                                           0;
                                                                                                    Gaps
                                                                                                    0;
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В

Swiss Institute of Bioinformatics

and the

EMBL outstation

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RA Ghim S.Y., Glaser P., Goffead M., Found S., Gallghtly E.J., Grandi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Ra Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Goris B., Karamata D., Kasahara Y., Klaerr Blanchard M., Klein C., RA Guiser B., Lepidus A., Lardinois S., Lauber J., Lazarevic V., RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Ra Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., RA Lee S.M., Levine A., Ugiwara A., Oudega B., Park S.H., RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., RA Presecan E., Pujic P., Purnelle B., Roche B., Rose M., Sadaie Y., Schleich S., Schroeter R., Sooffone F., Schina E., Schleich S., Schroeter R., Sooffone F., Schina E., Schleich S., Schroeter R., Sooffone F., Sould B., Takagi T., Takahashi H., Takemaru K., Takochi M., Tamakoshi A., Taroka T., Terpstra P., Tognoni A., RA Takeuchi M., Tamakoshi A., Taroka T., Terpstra P., Tognoni A., RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Woshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., The Complete genome sequence of the Gram-positive bacterium Bacillus RT subtills.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
YJLD_BACSU
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                  regulation map for Bacillus subtilis.", Electrophoresis 18:1451-1463(1997).
-!- COFACTOR: FAD (BY SIMILARITY).
                                                                                       -!- INDUCTION: BY GLUCOSE STARVATION.
                                                                                                                                                                                                                                                                                                                                                                     Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=168 / IS58;
MEDLINE=97443988; PubMed=9298659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghimm S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G., Ghimm S.Y., Glaser D., Goffeau A., Gollightly E.J., Grandi G., Grita M., Glaser D., Goffeau A., Gollightly E.J., Grandi G., Grita M., Glaser D., Goffeau A., Gollightly E.J., Grandi G., Grita M., Grita M., Grandi G., Grita M., Grandi G., Grita M., Grandi G., Grita M., Grandi G., Grita M., Grita M., Grita M., Grandi G., Grita M., Grandi G., Grita M., Grit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rivolta C., Soldo B., Lazarevic V., Joris B., Mauel C., Karamata D., "A 35.7 kb DNA fragment from the Bacillus subtilis chromosome containing a putative 12.3 kb operon involved in hexuronate catabolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microbiology 144:877-884(1998).
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15-JUN-2002 (Rel. 41, Last annotation update)
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-) (Glucose starvation-inducible protein 5) (GSI5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P80861; Q9R442;
01-NOV-1997 (Re
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                                                                                                                                                                                                                                                                                      steps from a two-dimensional protein index towards a response
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Batter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pfam; pf00070; pyr_redox; 1.
pRINTS; pR00368; FADPNR.
pRINTS; pR00411; pNDRDTASEI.
proDom; pD000139; FAD_pyr_redox; 1.
oxidoreductase; Flavoprotein; FAD; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SubtiList; BG13203; yjlD.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001100; Pyr_redox.
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09V3J1: 09VJV2;

16-CCT-2001 (Rel. 40, Created)

16-CCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

16-CCT-2001 (Rel. 41, Last annotation update)

18-JUN-2002 (Rel. 41, Last annotation update)

Vacuolar ATP synthase subunit H (EC 3.6.3.14) (V-ATPase H subunit)

Vacuolar proton pump H subunit) (Vacuolar proton pump subunit SFD (Vacuolar proton pump SFD (Vacuolar Proton pump SFD (Vacuolar Proton pump SFD OR CG17332.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muscomorpha; Ep
NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of vhaSFD, the gene encoding a SFD subunit of the Drosophila V-ATPAse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 VLPDDLIE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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75.0%;
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Pred. No.
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Y284_AQUAE

066638;

Y284_AQUAE

STANDARD;

PRT;

440 AA.

0;

30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)

Hypothetical protein AQ_284.

Aquifex aeolicus

NCBI_TaxID=63363

Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;

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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F. N., Rubin G.M., Venter J.C.,
RA Zheng X.H., Zhong F. N., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster.",
RT "Genome sequence of Drosophila melanogaster.",
RT SCience 287:2185-2195(2000).
RL Science 287:2185-2195(2000).
Science 287:2185-2195(2000).
Science 287:2185-2195(2000).
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RESULT 16
                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                                                                                                        Pfam; PF03224; V-ATPase_H;
                                                                                                                                                                                                                                                                                                                                                                    interpro;
                                                                                                                                                                                                             Local
                                                                               79 VLIDDLLQ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELLS, THUS PROVIDING MOST OF THE ENERGY REQUIRED FOR TRANSPORT PROCESSES IN THE VACUOLAR SYSTEM (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(In) = ADP + phosphate +
                                                                                                                                   1 VLXDDLLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c^{\,\prime\,\prime} and d). SIMILARITY: BELONGS TO THE V-ATPASE H SUBUNIT FAMILY. CAUTION: Ref.2 sequence differs from that shown due t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: V-Arpase is an heteromultimeric enzyme composed of a peripheral catalytic V1 complex (components A to H) attached to an integral membrane V0 proton pore complex (components: a, c, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                             AF159457; AAD47254.1;
AE003652; AAF53555.2;
AE003652; AAF53556.2;
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                 IPR004908; V-ATPase_H
                                                                                                                                                                                                                                                                                    ATP synthesis;
392 AA; 45159
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                               45159 MW;
                                                                                                                                                                                                                  76.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    VhaSFD.
                                                                                                                                                                                                                                                                                               Hydrogen ion transport.
MW; B7F6E1BB712F4305 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          ALT_SEQ.
                                                                                                                                                                                                                  Score 29; DB 1;
Pred. No. 1.1e+02;
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                 Length 392;
                                                                                                                                                                                                     0;
                                                                                                                                                                                                       Gaps
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YS02_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                          SEQUENCE
                                                  Hypothetical protein
                                                                WormPep; ZK1128.2; CE01684.
                                                                              EMBL; 247357; CAA87421.1;
                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                   Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea.
                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                 ZK1128.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS; TIGRUUUBS; UFLOCK.,
PROSITE; PS01278; UPP0004; 1.
PROSITE; PS01278; UPP0004; 1.
Prothetical protein; Complete proteome.

Hypothetical protein; Complete proteome.

Hypothetical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical 55.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         209357;
                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00919; UPF0004; 1.
Pfam; PF01938; TRAM; 1.
TIGREAMS; TIGR00089; UPF0004; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000682; AAC06605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V., The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 LTDDIIEA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002792; TRAM.
InterPro; IPR001861; UPF0004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 392:353-358(1998).
-!- SIMILARITY: BELONGS TO THE UPF0004 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     -NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                              Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 40, Last annotation update) kDa protein ZK1128.2 in chromosome III.
                                     55549 MW;
                                                                                                                                              institutions as long as its content
         76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.3%;
62.5%;
    Score 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29;
Pred. No. 1
                               BCB23D2766188D4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 AA.
 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2e+02;
                                                                                                                                Usage by
Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                  and
                                                                                                                                                1S
                                                                                                                              for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                              no
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DЪ
                                                                                                                                                                                                                                                                                      LEPA_BORBU
                                                                                                                                      RESULT 19
                                                                                                                                                                                                       ζ
                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 18
                                                   15-DEC-1998
15-DEC-1998
16-OCT-2001
Borrelia burgdorferi (Lyme disease spirochete)
                        GTP-binding pro
LEPA OR BB0088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
                                                                                             051115;
                                                                                                                                                                                                                                                                                        Hydrolase; Glycosidase; Polysaccharide degradation.
ACT_SITE 102 102
BY SIMILARITY
ACT_SITE 187 187 BY SIMILARITY.
                                                                                                          LEPA_BORBU
                                                                                                                                                                            472 DDLLEA 477
                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                               PROSITE: PS00506; BETA_AMYLASE_1; 1.
PROSITE: PS00679; BETA_AMYLASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00750; BETAAMYLASE
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01373; Glyco_hydro_14; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF049098; AAD04259.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001554; GH_14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polysaccharides so as to remove successive maltose units non-reducing ends of the chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: CATALYZES THE LIBERATION OF MALTOSE FROM 1,4-ALPHA-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallagher J., Gana J.A., Pollock C., Cunningham S.M., Volenec J.J.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Trifolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC 1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trifolium repens (Creeping white clover)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 065015;
                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMYB_TRIRP
                                                                                                                                                                                                      4 DDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 LLIDDLLKA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BETA-AMYLASES).
                                                                                                                                                                                                                                                                                                                                                                                                         P10538;
                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 6; Conserv
                                                                                                                                                                                                                                                                                   496 AA;
                                        (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
                                    protein lepa.
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                56088 MW;
                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                        76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%;
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                        Score 29;
Pred. No.
                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                            8FC446AB7C927F19 CRC64;
                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                   606 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496 AA
                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                      1.4e+02
                                                                                                                                                                                                                                               Length 496;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosidae;
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                   0,
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                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98065943; PubMed=9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPRO04161; EFTU_D2:
Interpro; IPRO00795; EF_GTPbin:
Interpro; IPRO05225; Small_GTP
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P13551; 1ELO.
TIGR; BB0088; -.
                                                                                                                                                                                     Q9EPU4;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Cleavage and polyadenylation specificity factor, 160 kDa subunit (CPSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
                                                                                                                                                                                                                                                                  CPSA_MOUSE
MEDLINE=21261509; PubMed=11369601;
Dass B., Attaya E.N., Michelle Wallace A., MacDonald C.C.;
"Overexpression of the CstF-64 and CPSF-160 polyadenylation protein
                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                         CPSF1
                                                  TISSUE=Testis
                                                               SEQUENCE FROM N.A.
                                                                                           NCBI_TaxID=10090;
                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                             178 DDLLEA 183
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           4 DDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEPA SUBFAMILY.
                                                                                                                                                                          kDa subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE001121; AAC66469.1; ALT_INIT.
                                                                                                                                                         OR CPSF160.
                                                                                                             lia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                          6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR00231; small_GTP; 1. ps00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35210 / B31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        606 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome
                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68172 MW;
                                                                                                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EF_GTPbind
                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         76.3%; Score 29; DB 1; L
100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _GTP.
                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTP
                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                               sciurognathi;
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29E9F10445246255 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                         1441 AA
                                                                                                                  Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 606;
                                                                                                                     Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E.K., Gwinn M.,
                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  0
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    messenger RNAs in mouse male germ cells.";
Biol Reprod. 64:1722-1729(2001).
-i- FUNCTION: CPSF PLAYS A KEY ROLE IN PRE-MRNA 3'-END FORMATION,
-I- FUNCTION: CPSF PLAYS A KEY ROLE IN PRE-MRNA 3'-END FORMATION,
RECOGNIZING THE AGUANA SIGNAL SEQUENCE AND INTERACTING WITH
POLY(A)POLYMERASE AND OTHER FACTORS TO BRING ABOUT CLEAVAGE AND
POLY(A) ADDITION. THIS SUBBUNIT IS INVOLVED IN THE RNA RECOGNITION
STEP OF THE POLYADENYLATION REACTION (By similarity).
-i- SUBBUNITS 160, 100, 70 AND 30 kDa.
SUBBUNITS 160, 100, 70 AND 30 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1426 IILDDLLE 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA processing; Nu SEQUENCE 1441 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004871; CPSF_A. Pfam; PF03178; CPSF_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF322193; AAG40326.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Cleavage and polyadenylation specificity factor, 160 kDa subunit (CPSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPSF1 OR CPSF160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q10570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPSA_HUMAN
                                                                                                                                                                  POLY(A) ADDITION. THE SUBUNIT IS INVOLVED IN THE RACORITION,
POLY(A) POLYMERASE AND OTHER RACTORS TO BRING ABOUT CLEAVAGE AND
POLY(A) ADDITION. THIS SUBUNIT IS INVOLVED IN THE RNA RECOGNITION
STEP OF THE POLYADENYLATION REACTION.
1. SUBUNIT: CPSF IS A HETEROTETRAMER COMPOSED OF FOUR DISTINCT
SUBUNITS 160, 100, 70 AND 30 kDa.
1. SUBCELLULAR LOCATION: NUCLear; nucleoplasm.
                                                                                                                                                                                                                                                                                                                          Murthy K.G., Manley J.L.;
"The 160-kD subunit of human cleavage-polyadenylation specificity factor coordinates pre-mRNA 3'-end formation.";
Genes Dev. 9:2672-2683(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                    Genes Dev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 kDa subunit
                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96067159; PubMed=7590244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VLXDDLLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNITS 160, 100, 70 AND 30 kDa.
SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM (By similarity).
SIMILARITY: BELONGS TO THE CPSF160 FAMILY.
                                                                                                                                  PTM: THE N-TERMINUS IS BLOCKED. SIMILARITY: BELONGS TO THE CPSF160 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ს</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein; RNA-binding
NA; 160817 MW; 5D927224152A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB 1;
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5D927224152AC3B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1442 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1441;
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                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
mRNA processing; Nuclear protein; RNA-binding.
                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                       Keller W., Bienroth S., Lang K.M., Christofori G.,

"Cleavage and polyadenylation factor CPF specifically interacts with
the pre-mRNA 3' processing signal AAUAAA.";

EMBO J. 10:4241-4249(1991)

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FUNCTION: CPSF PLAYS A KEY ROLE IN PRE-MRNA 3'-END FORMATION,
RECOGNIZING THE AAUAAA SIGNAL SEQUENCE AND INTERACTING WITH
POLY(A)POLYMERASE AND OTHER FACTORS TO BRING ABOUT CLEAVAGE AND
POLY(A) ADDITION. THIS SUBUNIT IS INVOLVED IN THE RNA RECOGNITION
STEP OF THE POLYADENYLATION REACTION.
                                                 EMBL; X83097; CAA58152.1; -.
                                InterPro; IPR004871; CPSF_A.
                                                                                                                                                                                        -!- PTM: THE N-TERMINUS IS BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Jenny A., Keller W.; "Cloning of cDNAs encoding the 160 kDa subunit of the bovine cleavage and polyadenylation specificity factor."; Nucleic Acids Res. 23:2629-2635(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92097544; PubMed=1756731;
                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95380277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPSF1 OR CPSF160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPSA_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q10569;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA processing; Nuclear protein; RNA-binding.
DOMAIN 893 908 NUCLEAR LOCALIZAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004871; CPSF_A.
Pfam; PF03178; CPSF_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U37012; AAC50293.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leavage and polyadenylation specificity factor, 160 kDa subunit (CPSF
                                                                                                                                                                                                                SUBUNIT: CPSF IS A HETEROTETRAMER COMPOSED OF FOUR DISTINCT SUBCELLULAR LOCATION: Nuclear; nucleoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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               PF03178; CPSF_A; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=7651824;
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62.5%;
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                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                            There are no restrictions on ong as its content is in no
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                                                                                                  Usage
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FER_BACTH
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Best Local
          Fukuyama K.,
               X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS). MEDLINE=88172459; PubMed=3351918;
                                                                                                01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                 Bacillus thermoproteolyticus, Bacillaceae; Bacillus Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus NCBI_TaxID=1427;
                                                                                          Ferredoxin
                                                                                                                                         P10245;
                                                                                                                                                   FER_BACTH
                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                          METAL
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                                                                                                                                                                                                                                                                                                                                                            METAL
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                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR001080; 3Fe4S_ferredoxin.
InterPro: IPR001450; 4Fe4S_ferredoxin.
                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                               PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS
-!- COFACTOR: BINDS 1 4FE-4S CLUSTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from Bacillus stearothermophilus."; Biochem. J. 159:55-63(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hall D.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hase T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Geobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P00212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ferredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FER_BACST
                                                                                                                                                                                                              49 ILIDDMMDA
                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a four-iron-four-sulphur ferredoxin isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                     1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 62.5%; les 5; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                         PR00352; 3FE4SFRDOXIN.
                                                                                                                                                                                                                                                                                                                                                                          PS00198; 4FE4S_FERREDOXIN; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohmiya N., Matsubara H., Mullinger R.N., Rao K.K.,
                                                                                                                                                                                                                                                                                                           81 AA;
                                                                                                                                                                                                                                                             Conservative
        Nagahara
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                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                        8770 MW;
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                                                                                               Last annotation update)
                                                                                                             Last sequence update)
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Tsukihara T., Katsube Y., Hase T.,
                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                 IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
                                                                                                                                                                                                                                                                    Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                     C5FDE6EB193A525C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2:
                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29; Pred. No. 4.4e+02; 1;
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W: 226B3A4F9812E0FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                               81 AA.
                                                                                                                                                                                                                                                                   DB 1; Length 81; 32;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fukuyama K., Okada T., Kakuta Y., Takahashi Y.;
"Atomic resolution structures of oxidized [4Fe-4S] ferredoxin from Bacillus thermoproteolyticus in two crystal forms: systematic distortion of [4Fe-4S] cluster in the protein.";
J. MOI. Biol. 315:1155-1166(2002).
-!- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (0.92 ANGSTROMS). MEDLINE=21686305; PubMed=11827483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukuyama K., Matsubara H., Tsukihara T., Katsube Y.; "Structure of [4Fe-4S] ferredoxin from Bacillus thermoproteolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90096160; PubMed=2600971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsubara H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS. -I- COFACTOR: BINDS 1 4FE-4S CLUSTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 refined at 2.3-A resolution. Structural comparisons of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; 11R0; 13-FEB-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ferredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Tertiary structure of Bacillus thermoproteolyticus
                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L7/L12.
RPLL OR RSC3035 OR RS04722.
                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       TURN
                                                                                                                                                                                                                                                                                                                                                                                                       TURN
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001080; 3Fe4S_ferredoxin.
InterPro; IPR001450; 4Fe4S_ferredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ferredoxins.";
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                                                                                                                                                                                                                                                                                                                              STRAND
                                                                                                                                                                                                                                                                                                                                                                  HELIX
                                                                                                                                                                                                                                                                                                                                                                                           STRAND
                         Ralstonia
                                     Bacteria; Proteobacteria;
                                               Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                     RL7_RALSO
          NCBI_TaxID=305;
                                                                                                                           Q8XUZ7;
                                                                                                                                                                                                    49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Biol. 199:183-193(1988).
                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                            1 VLXDDLLEA 9
                                                                                                                                                                                                 ILIDDMMDA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO0352; 3FE4SFRDOXIN.
; PS00198; 4FE4S_FERREDOXIN; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. 210:383-398(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evolutionary implications for bacterial ferredoxins.";
                                                                                                                                                                                                                                                                                                     81 AA;
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                     8770 MW;
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17
61
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11 IRON-SULFUR
                                                                                                                                                                                                                                                               44.48;
                                                                                                                                                                                                                                                                           73.7%;
                                      beta
                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                     C44C3D9B193A525C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
                                                                                                                                                                                                                                                                           Score 28;
                                                                                                                                                                                                                                                                 Pred. No. 32;
                                                                                                                                       PRT;
                                     subdivision;
                                                                                                                                        124 AA
                                                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (4FE-4S).
                                      Ralstonia group;
                                                                                                                                                                                                                                                                             Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-structure.
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NIKR_ECOLI
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1- FUNCTION: Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD001326; Ribosom
TIGRFAMs; TIGR00855; L12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      P28910; Q47559;

01-DEC-1992 (Rel. 24, Created)

01-DEC-1992 (Rel. 24, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., SEQUENCE OF 1-7, AND CHARACTERIZATION MEDLINE-99102235; PubMed=9882686;
                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli, and
Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                     Nickel responsive regulator.
NIKR OR B3481 OR Z4873 OR ECS4348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00542; Ribosomal_L12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                 MEDLINE=93259920; PubMed=8387990; Zhao S., Sandt C.H., Feulner G., Vlazny D.A., Gray J.A., Hill C.W.; "Rhs elements of Escherichia coli K-12: complex composites of shared
                                                                                                                              STRAIN=K12
                                                                                                                                                                                              "Isolation and characterization of the nikR gene encoding a nickel-responsive regulator in Escherichia coll.";
                                                                                                                                                                                                                                                    De Pina K., Desjardin
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
 SEQUENCE FROM N.A
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                Bacteriol, 181:670-674(1999).
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3 ITKDDILEA 11
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es 5; Conserv
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                                  Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS
                              unique components that have different evolutionary histories."; Bacteriol. 175:2799-2808(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; Complete proteome 124 AA; 12520 MW; 271C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribosomal_L12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.7%;
                                                                                                                                                                                                                                                        V., Mandrand-Berthelot M.-A., Giordano G.,
                                                                                                                                                                                                                                                                                                                                                                   gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                 "Regulation of high affinity nickel uptake in bacteria. Ni2+-dependent interaction of NikR with wild-type and mutant operator sites.";
J. Biol. Chem. 275:19735-19741(2000).
                                                                                                                                                                                                                                                                                                                                                                                          Chivers P.T., Sauer R.T.;
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12 / MC1061;
MEDLINE=20347879; PubMed=10787413;
                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chivers P.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20061003; PubMed=10595554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulation of their expressions: an applicable procedure for genomic analysis of other microorganisms.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Scherichia coli "Complete genome sequence of enterohemorrhagic Escherichia coli ol57:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=K12 / W3110;
MEDLINE=94162733; PubMed=7764507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94316500; pubMed-8041620;
Sofia H.J., Burland V., Daniels D.L., Plur
"Analysis of the Escherichia coli genome.
region from 76.0 to 81.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "NikR is a ribbon-helix-helix DNA-binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:529-533(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 22:2576-2586(1994).
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                                                                                                                                                European Bioinformatics Institute.
                                                                                                                                                                                                                                        SIMILARITY:
                                                                                                                                                                                                                        REGULATORS.
                                                                                                                                                                                                                                                         SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                  COFACTOR: Binds 1 nickel ion per subunit
                                                                                                                                                                                                                                                                                        active in the presence of excessive intracellular nickel.
                                                                                                                                                                                                                                                                                                                      FUNCTION: Transcriptional repressor of the nikABCDE
          Y08952; CAA70150.1; -. L02370; AAC61882.1; -. U00039; AAB18456.1; -.
   AE000423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biotechnol. Biochem. 58:117-120(1994)
                                                                                            requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         products of the Escherichia coli genomic genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8:2494-2500(1999).
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                                                                                                                                                                                                                               BELONGS TO THE COPG/NIKR FAMILY OF TRANSCRIPTIONAL
AAC76506.1;
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                                                                                                                                                               Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Hollroyd S., Jägels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skalton T., Parry C.,
                                                                                               "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
   This SWISS-PROT entry is copyright.
                                          -!- SUBUNIT: Homodimer (
                                                                     -!- FUNCTION: Transcriptional regulator (Potential).
-!- COFACTOR: Binds 1 nickel ion per subunit (By similarity).
                                                                                                                                                    Whitehead
                                                                                                                                                                                                                                                                SPECIES=S.typhi; STRAIN=CT18; MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                           McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SALTY
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
MUTAGEN
                                                                                                                                                                                                                                                                                                                         Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                    Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=602,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nickel responsive regulator. NIKR OR STM3584 OR STY4227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8XEK6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; DNA-binding; Repressor;
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                                  REGULATORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE005572; AAG58608.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                 S., Barrell B.G.;
                                                                                                                                                            Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002145; CopG_HTH_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AA;
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                                        (By similarity).
S TO THE COPG/NIKR FAMILY OF TRANSCRIPTIONAL
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NICKEL (POTENTIAL).
R->A: LOSS OF DNA-BINDING.
KE -> EGRLSLLLGPLVN (IN RE
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produced through a collaboration
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RX KEDLINE-98044033; PubMed=9384377;
RX KEDLINE-98044033; PubMed=9384377;
RA KUNST F., Oggaswara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Cappano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Cappano V., Carter N.M.,
RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Entian K.D., Errington J., Fabrett C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Coffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosson S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Kosamata D., Kasahara Y., Klaerr-Blanchard M., Klelin C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Laber J., Lazarevic V.,
RA Median N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Median N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parsocan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL627281; CAD08046.1; -. StyGene; SG?????; nikR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95219083; PubMed=7704258; Albertini A.M., Caramori T., Scoffone F., Scotti C., Ga "Sequence around the 159 degree region of the Bacillus genome: the pks% locus spans 33.6 kb.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; DNA-binding; Nickel; Metal-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microbiology 141:299-309(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 AA;
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(Rel. 31, Last sequence update)
(Rel. 41, Last annotation update)
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Pred. No. 55;
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NICKEL (POTENTIAL).
NICKEL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U11039; AAA85142.1; -.
EMBL; Z99112; CAB13588.1; -.
EMBL, Z99113; CAB13599.1; -.
Subtilist; BG10928; pksI.
InterPro; IPR001753; EnCoA_hydrtse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                   Ortin J., Martinez C., del Rio L., Davila M., Lopez-Galindez C., Villanueva N., Domingo E.;
Villanueva N., Domingo E.;
"Evolution of the nucleotide sequence of influenza virus RNA segment "Evolution of the nucleotide sequence of influenza virus RNA segment 7 during drift of the H3N2 subtype.";
Gene 23:233-239(1983).
Gene 23:233-239(1983).
-i- FUNCTION: THIS PROTEIN FORMS A CONTINUOUS SHELL ON THE INNER SIDE OF THE LIPID BILAYER. MAINTAINS THE STRUCTURAL INTEGRITY OF THE VIRUS PARTICLE THROUGH HYDROPHOBIC INTERACTIONS. ALSO MEDIATES THE ENCAPSIDATION OF RNA NUCLEOPROTEIN CORES INTO THE MEMBRANE THE ENCAPSIDATION OF RNA NUCLEOPROTEIN CORES INTO THE MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibiotic biosynthesis; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                   Influenza A virus (strain A/Bangkok/1/79)
Viruses; ssRNA negative-strand viruses; O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P03487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matrix protein M1.
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                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=11325;
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                                                                                                                                                                                                                                                                                                                  MEDLINE=84005895; PubMed=6688599;
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                                                              ALTERNATIVE PRODUCTS: MATRIX PROTEINS M1 AND M2 ARE PRODUCED BY ALTERNATIVE SPLICING OF RNA SEGMENT 7. ONLY THE FIRST 9 RESIDUES
                                            ARE SHARED BY THE TWO PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00378; ECH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 AA;
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entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                        Influenzavirus
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Pred. No. 1.1e+02;
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                               Matrix protein; RNA-binding; Alternative splicing SEQUENCE 252 AA; 27964 MW; F4091A18C48C9800 C
                                                                                                      SEQUENCE
                                                                                                                                          Pfam; PF00598; Flu_M1; 1. ProDom; PD001061; Flu_M1; 1.
                                                                                                                                                                                                                                                                                               entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 PIR; B45539; B45539.
HSSP; P03485; 1AA7.
                                                                                                                                                                                                                                                         EMBL; L37795; AAA56804.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klimov A., Proesch S., Schaefer J., Bucher D., "Subtype H7 influenza viruses: comparative antigenic and molecular analysis of the HA-, M-, and NS-genes.";

Arch. Virol. 122:143-161(1992).
                                                                                                                                                                                         InterPro; IPR001561; Flu_M1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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SEQUENCE 252 AA; 27810 MW; F892297A838486C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Influenza A_virus (strain A/Chicken/Brescia/1902)
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ProDom; PD001061; Flu_M1; 1.
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HSSP; P03485; 1AA7
                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: THIS PROTEIN FORMS A CONTINUOUS SHELL ON THE INNER SIDE OF THE LIPID BILAYER. MAINTAINS THE STRUCTURAL INTEGRITY OF THE VIRUS PARTICLE THROUGH HYDROPHOBIC INTERACTIONS. ALSO MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: MATRIX PROTEINS MI AND M2 ARE PRODUCED BY ALTERNATIVE SPLICING OF RNA SEGMENT 7. ONLY THE FIRST 9 RESIDUES
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              Similarity 6; Conserv
           Conservative
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                            73.7%;
85.7%;
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PIR; S04060; S04060
PIR; S14616; S14616
HSSP; P03485; 1AA7
Influenza A virus (strain A/Fowl plague virus/Rostock/34).
                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq.
15-JUL-1998 (Rel. 36, Last anno
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                         Matrix protein M1
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Pfam; PF00598; Flu_M1; 1.

ProDom; PD001061; Flu_M1; 1.

Matrix protein; RNA-binding; Alternative splicing.

Matrix protein; RNA-binding; 7317397B86DFC877 CRC64;
                                                                                            P03488;
                                                                                                          VMT1_IAFPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequences of influenza A virus RNA segment 7: a comparison of five isolates.";
Nucleic Acids Res. 17:2870-2870(1989).
-!- EUNCTION: THIS PROTEIN FORMS A CONTINUOUS SHELL ON THE INNER SIDE OF THE LIPID BILAYER. MAINTAINS THE STRUCTURAL INTEGRITY OF THE VIRUS PARTICLE THROUGH HYDROPHOBIC INTERACTIONS. ALSO MEDIATES
                                                                                                                                                                                         229 LKDDLLE 235
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001561; Flu_M1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89240054; PubMed=2701939;
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"Nucleotide sequence of fowl plague virus RNA segment 7.";
J. Gen. Virol. 58:211-215(1982).
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01-NOV-1988 (Rel.
15-JUL-1998 (Rel.
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ProDom; PD001061; Flu_M1; 1.
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MEDLINE=88221675; PubMed=3450279; Karginov V.A., Blinov V.M., Safronov P.F., Mamaev L.V., Golwetesov S.V., Samokhvalov E.I., Sharova N.K., Yuferov V.P., Urivaev L.V., Bukrinskaya A.G.; "Comparative analysis of primary structure of M-genes in reresistant and remantadine-sensitive strains of influenza vi
                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence of RNA segment 7 and the predicted amino sequence of M1 and M2 proteins of FPV/Weybridge (H7N7) and WS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88323193; PubMed=3414185;
Markushin S., Ghiasi H., Sokolov N., Shilov A., Sinitsin B., Brown D.,
Klimov A., Nayak D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P05775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAFPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=11384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Influenza A virus (strain A/Fowl plague virus/Weybridge).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matrix protein Ml
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                influenza viruses
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FUNCTION: THIS PROTEIN FORMS A CONTINUOUS SHELL ON THE INNER SIDE OF THE LIPID BILAYER. MAINTAINS THE STRUCTURAL INTEGRITY OF THE VIRUS PARTICLE THROUGH HYDROPHOBIC INTERACTIONS. ALSO MEDIATES VIRUS PARTICLE THROUGH HYDROPHOBIC INTERACTIONS. ALSO MEDIATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.7%;
85.7%;
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Pred. No. 1.1e+02;
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                       of influenza virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (H7N7) and WSN (H1N1)
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                                                                                                                                                                                                   Golovin S.Y.,
                                                                     remantadine
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Query Match
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Bioorg, Khim. 13:1638-1643(1987).

-i- FUNCTION: THIS PROTEIN FORMS A CONTINUOUS SHELL ON THE INNER SIDE
OF THE LIPID BILAYER. MAINTAINS THE STRUCTURAL INTEGRITY OF THE
VIRUS PARTICLE THROUGH HYDROPHOBIC INTERACTIONS. ALSO MEDIATES
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                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1988 (Rel. 01-AUG-1988 (Rel. 01-AUG-1988 (Rel. 01-AUG-1998 (Rel. 015-JUL-1998 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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PIR; PN0086; PN0086.
PIR; S07945; S07945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M23917; AAA43251.1; -.
EMBL; M38299; AAA43314.1; ALT_TERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VMT1_IAMAN P08381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00598; Flu_M1; 1. ProDom; PD001061; Flu_M1; 1.
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                   Buckler-White A.J., Naeve C.W., Murphy B.R.;

"Characterization of a gene coding for M proteins which is involved in host range restriction of an avian influenza A virus in monkeys.";

J. Virol. 57:697-700(1986).

-I- FUNCTION: THIS PROTEIN FORMS A CONTINUOUS SHELL ON THE INNER SIDE OF THE LIPID BILAYER. MAINTAINS THE STRUCTURAL INTEGRITY OF THE OF THE LIPID BILAYER.
                                                                                                                                                                                                                                                                                                                                                                    Matrix protein M1
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                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                             Influenza A virus (strain A/Mallard/New York/6750/78)
                                                                                                                                                                                       MEDLINE=86115422; PubMed=3080604;
                                                                                                                                                                                                                                                              NCBI_TaxID=11435;
                                                                                                                                                                                                                                                                                       Influenza A viruses; Influenzavirus
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 LKDDLLE 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENVELOPE
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VIRUS PARTICLE THROUGH HYDROPHOBIC INTERACTIONS. ALSO MEDIATES
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                                                                                                                                                                                                                                                                                                                                                                                                   08, Created)
08, Last sequence update)
36, Last annotation update)
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F -> L (IN REMANTADINE L -> I (IN REF 2).

V -> A (IN REF 2).

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S -> A (IN REF 2).

K -> R (IN REF 2).

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-> R (IN REF. 2).
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-> H (IN REF. 2).
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"Nucleotide sequences of influenza A virus RNA segment 7: a comparison of five isolates."; Nucleic Acids Res. 17:2870-2870(1989).
-!- FUNCTION: THIS PROTEIN FORMS A CONTINUOUS SHELL ON THE INNER SIDE OF THE LIPID BILAYER. MAINTAINS THE STRUCTURAL INTEGRITY OF THE
                                                                                                          SEQUENCE FROM N.A.
STRAIN=A/Port Chalmers/1/73;
MEDLINE=89240054; PubMed=2701939;
                                                                                            Zebedee S.L., Lamb R.A.;
                                                                                                                                                                              protein (M2) in H1N1 and H3
Virology 112:746-751(1981).
                                                                                                                                                                                   "Conservation of the influenza virus membrane protein (M1) amino acid sequence and an open reading frame of RNA segment 7 encoding a second protein (M2) in H1N1 and H3N2 strains.";
                                                                                                                                                                                                                                                                                                                                                       Lamb R.A., Lai C.-J., Choppin P.W.;
"Sequences of mRNAs derived from genome RNA segment 7 of influenza virus: colinear and interrupted mRNAs code for overlapping
                                                                                                                                                                                                                                                MEDLINE=81251059; PubMed=7257189; Lamb R.A., Lai C.-J.;
                                                                                                                                                                                                                                                                                   STRAIN=A/Udorn/307/72;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Influenza A virus (strain A/Udorn/307/72), and Influenza A virus (strain A/Port Chalmers/1/73).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=82037801; PubMed=6945577;
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A/Udorn/307,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-13 AND 210-252 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11480,
                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 78:4170-4174(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matrix protein M1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P03486; P10919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matrix protein; RNA-binding; Alternative splicing. SEQUENCE 252 AA; 27926 MW; A9E238FAC2044A45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAUDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00598; Flu_M1; 1. ProDom; PD001061; Flu_M1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M12699; AAA43313.1; -. PIR; A29511; MFIV1M. HSSP; P03485; 1AA7.
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Best Local Similarity
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P05777;
01-NOV-1988 (Rel. 0
01-JUL-1989 (Rel. 1
15-JUL-1998 (Rel. 3
Baylor N.W., Zhiping Y.L., Wagner R.R.; "Transient expression and sequence of the matrix (M1) gene of WSN influenza A virus in a vaccinia vector."; Virology 163:618-621(1988).
                                                                                                            SEQUENCE FROM N.A.
MEDLINE=88179567; PubMed=3354209;
                                                                                                                                                                                                                                    "Nucleotide sequence of RNA segment 7 and the predicted amino sequence of M1 and M2 proteins of FPV/Weybridge (H7N7) and WS influenza viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A94326; METVC.
PIR; S04058; S04058.
PIR; S04054; S04054.
HSSP; P03485; lAA7.
                                                                                                                                                                                                                                                                                                                               Markushin S., Ghiasi H., Sokolov N., Shilov A., Sinitsin Klimov A., Nayak D.;
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88323193; PubMed=3414185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=89240054; PubMed=2701939;
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                                                                                                                                                                                                                     Virus Res.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 17:2870-2870(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequences of influenza A virus RNA segment 7: comparison of five isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA negative-strand viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zebedee S.L., Lamb R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11487
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ProDom; PD001061; Flu_M1; 1.
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VARIANT 41 41 A -> V (IN MOUSE-ADAR
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                                                                                                                                                                                                         10:263-272(1988).
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36,
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27804 MW;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                       01-NOV-1988
01-NOV-1988
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                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=85042103; PubMed=6495656;

Nakajima K., Nobusawa E., Nakajima S.;

"Genetic relatedness between A/Swine/Iowa/15/30(HlN1) and human influenza viruses.";
                                                                                                                                                                                                                                                                                           Influenza A virus (strain A/Swine/Iowa/15/30).
Viruses; ssRNA negative-strand viruses; Orthom
                                                                                                                                                                                                                                                                                                                          Matrix protein M1.
                                                                                                                                                                                                                                                                                                                                        01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
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                                                                                                                Influenza A viruses; Influenzavirus
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S04050; S04050.
S07429; S07429.
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                                                         ALTERNATIVE PRODUCTS: MATRIX PROTEINS M1 AND M2 ARE PARTERNATIVE SPLICING OF RNA SEGMENT 7. ONLY THE FIRST
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ARE SHARED BY THE TWO PROTEINS.
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SWISS-PROT entry is copyright. It is produced through a collaboration een the S_{w} is S Institute of Bioinformatics and the EMBL outstation -
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M23920; AAA43252.1; ALT_SEQ.
M19374; AAA43352.1; -.
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219 I
231 D
27864 MW;
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85.7%;
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Pred. No.
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I -> V (IN REF. 3).
D -> S (IN REF. 2).
                                                                                                     NUCLEOPROTEIN
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable encyl-CoA hydratase echa8 (EC 4.2.
ECHA8 OR ML2402 OR MLCB1306.05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                  "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: COULD POSSIBLY OXIDIZES FATTY AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1769;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECH8_MYCLE
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                                                                                                      EMBL; Y13803; C. EMBL; AL583925;
                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: (3S)-3-hydroxyacyl-CoA = trans-2(or 3)-enoyl-
                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE ENOYL-COA HYDRATASE/ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 LKDDLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LXDDLLE
                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: COULD POSSIBLY OXIDIZES FATTY ACIDS USING SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                     COMPONENTS (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                              CoA + H(2)0.
                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                       CAA74130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                          CAC31918.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flu_M1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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(EC 4.2.1.17).
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Pfam; PF00378; ECH; PROSITE; PS00166; EN Fatty acid metabolis

metabolism; Lyase; Complete

proteome

ENOYL_COA_HYDRATASE;

Leproma; ML2402;

IPR001753;

EnCoA_hydrtse

P14604; 2DUB.

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В
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Best Local
                                                                  InterPro; IPR000791; Grp1_Fun34_YaaH Pfam; PF01184; Grp1_Fun34_YaaH; 1. ProDom; PD010188; Grp1_Fun34_YaaH; 1
                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
 TRANSMEM
                              TRANSMEM
                                          Transmembrane
                                                      PROSITE; PS01114; GPR1_FUN34_YAAH;
                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         WEDLINE=95208539; runreur.//Volt M., Volckaert G.;
Verhasselt P., Aert R., Volckaert G.;
"Twelve open reading frames revealed in the 23.6 kb segment flanking
"Twelve open reading frames revealed in the 23.6 kb segment flanking
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288c / FY1679;
MEDLINE=95208356; PubMed=7900425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95028151; PubMed=7941739;
Lalo D., Stettler S., Mariotte S., Gendi
"Organization of the centromeric region
Saccharomyces cerevisiae.";
Yeast 10:523-533(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stettler S., Mariotte S., Riva M., Sentenac A., Thuriaux P., "An essential and specific subunit of RNA polymerase III (C) encoded by gene RPC34 in Saccharomyces cerevisiae."; J. Biol. Chem. 267:21390-21395(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Integral membrane protein (I-!- SIMILARITY: BELONGS TO THE GPR1/FUN34/YAAH FAMILY
                                                                                                                                                                                                                                                                                                                                                  Yeast 10:1355-1361(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUN34 protein.
FUN34 OR YNROO2C OR N2O29
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01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-GRF88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93016077; PubMed=1400451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VLXDDLL
                                                                                                                 S0005285; FUN34.
                                                                                                                               ; X63746; CAA45279.1; -.; X77395; CAA54571.1; -.; Z71617; CAA96278.1; -.; S31258; S31258.
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87
120
151
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85.7%;
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 POTENTIAL
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Pred. No. 1.1e+02;
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egion of chromosome
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                                                                                                                                                                                                                                                                                                                                 (Potential).
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RESULT 41
G3P_METJA
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Y32K_BNYVG
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STRAIN=JAL-1 / DSM 2661 / ATCC 43
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J.,
                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Clyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.59) (GAPD (NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase).
                                                                                                                                                                                             G3P_METJA STA
Q58546;
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
BOUZOUDAA S., Guilley H., Jonard G., Richards K.,
"Nucleotide sequence analysis of RNA-3 and RNA-4 o
yellow vein virus, isolates F2 and G1.";
J. Gen. Virol. 66:1553-1564(1985).
                                          SEQUENCE FROM N.A
                                                                               Archaea; Euryarchaeota; Methanococci; Met Methanocaldococcaceae; Methanocaldococcus
                                                                                                               Methanococcus jannaschii
                                                                                                                              GAP OR MJ1146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
01-NOV-1990 (Rel. 16, Last annotation update)
RNA-4 hypothetical 31.9 kDa protein.
Beet necrotic yellow vein mosaic virus (isolate
                                                                        NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
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01-NOV-1990
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                           DSM 2661 / ATCC 43067;
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G.J., Zhou L.,
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Fleischmann R.D.
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Best Local
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15-JUN-2002
15-JUN-2002
Peptidase B
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- CAMALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + pho-
- NAD(P)(+) = 3-phospho-D-glyceroyl phosphate + NAD(P)H.

- PATHWAY: Second phase of glycolysis; first step.
- SUBURIT: Homotetramer (By similarity).
- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
- SINCLARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Werrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
            Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Mexrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pfam; PF00044; gpdh; 1.
pfam; PF02800; gpdh_C; 1.
pROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPB_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycolysis; Oxidoreductase; NAD; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                          STRAIN=Rd / KWZU / AICC JIJU, MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPB OR HI0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 VSRDDILEA 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MJ1146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P10618;
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000173; GAP_dhdrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
(EC 3.4.11.-) (Aminopeptidase B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-PHOSPHATE
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   RESULT 43
PEPB_PASMU
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as Young ... usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9CM16;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update
15-JUN-2002 (Rel. 41, Last annotation update
Peptidase B (EC 3.4.11.-) (Aminopeptidase
PEPB OR PM1029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
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PROSITE; PS00631; CYTOSOL_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U32769; -; NOT_ANNOTATED_CDS.
TIGR; HI0875; -.
Asp or Glu residues (By similarity).
-!- COFACTOR: Manganese (By similarity).
-!- SUBUNIT: Homohexamer (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPB_PASMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .nterPro;
                                                                                                                                                                                                  'Complete
                                                                                                                                                                                                                                                               MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || | |:||
286 VLADGLIEA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VLXDDLLEA 9
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COPACTOR: Manganese (By similarity).
SUBUNIT: Homohexamer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SUMLLARITY: BELONGS TO PEPTIDASE FAMILY M17.
CAUTION: Ref. 1 sequence differs from that shown due to a frameshift in position 340. This may be a natural frameshift and
                                                                                  mplete genomic sequence of Pasteurella multocida Pm70."; c. Natl. Acad. Sci. U.S.A. 98:3460-3465(2016). role in intracellular FUNCTION: Probably plays an important role in intracellular peptide degradation. Hydrolyzes peptides with N-terminal acidic residues. The preferred substrates are peptides with N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Probably plays an important role in peptide degradation. Hydrolyzes peptides with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          this protein could be a pseudogene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000819; Peptidase_M17.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteobacteria; gamma
                                                                                                                                                                                                                                Zhang Q.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41, Last sequence update)
41, Last annotation update)
.4.11.-) (Aminopeptidase B).
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 1; Lo
Pred. No. 1.9e+02;
1; Mismatches 2;
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MANGANESE 2 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

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                                                                                                                                                                                                                                                                                                                                                                                                                                         subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 AA
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                                                                                                                                                                                                                                      Kapur V.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MALH_FUSMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    006901;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Maltose-6'.phosphate glucosidase (EC 3.2.1.122) (6-phospho-alpha-D-
                            SUBSTRATE SPECIFICITY STRAIN=ATCC 25557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=ATCC 25557; MEDLINE=97352666; PubMed=9209025;
                                                                                                                                                                                     phosphoryl-O-alpha-D-glucopyranosyl:6-phosphoglucohydrolase that hydrolyzes maltose 6-phosphate and related phospho-alpha-D-glucosides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bouma C.L., Reizer J., Reizer A., Robrish S.A., Thompson J., "6-phospho-alpha-D-glucosidase from Fusobacterium mortiferum: cloning, expression, and assignment to family 4 of the glycosylhydrolases.";
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-32, AND CHARACTERIZATION.
STRAIN-ATCC 25557;
                                                                                                                                                                                                                                                                                            Thompson J., Gentry-Weeks C.R., Nguyen N.Y., Folk J.E., Robi
Purification from Fusobacterium mortiferum ATCC 25557 of a
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95247687; PubMed=7730284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusobacterium mortiferum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00631; CYTOSOL_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; M17.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE006143; AAK03113.1; -. HSSP; P00727; 1LAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000819; Peptidase_M17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 VLADGLIEA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUSMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR00481; LAMNOPPTDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusobacteria; Fusobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Aminopeptidase; N 210 210 218 284 284 198 198 203 203 203 221 221 280 280 282 282 434 AA; 46877 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179:4129-4137(1997).
                                                                                                                                           177:2505-2512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptidase_M17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Manganese; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MANGANESE 2 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170A5FEA25AB9FB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                лв т,
1.9e+02;
2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 434;
                                                                                                                                                                                                                                                                                                                                     Robrish S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and for commercial
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RESULT 45
SYR_CORGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                Actinomycetales; Corynebacterineae; Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (Argrs).
ARGS OR CGL1179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NP_BIND
ACT_SITE
                                                  NCBI_TaxID=1718;
                                                                                                                                   Bacteria; Actinobacteria;
                                                                                                                                                           Corynebacterium glutamicum (Brevibacterium flavum)
                                                                                                                                                                                                                                                                                                                                            P35868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                          SYR_CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001088; GH_4.
Pfam; PF02056; Glyco_hydro_4; 1.
PRINTS; PR00732; GLHYDRLASE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carbohydrate metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Glycosidase; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01324; GLYCOSYL_HYDROL_F4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U81185; AAB63015.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Sucrose isomers and related alpha-linked glucosides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and gentobiose-6'P.
-i- CATALYTIC ACTIVITY: Maltose 6'-phosphate + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiology 148:843-852(2002) -1- FUNCTION: Hydrolyzes a wid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Metabolism of sucrose and its five isomers by Fusobacterium mortiferum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425 ILDDLIEA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pikis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO FAMILY 4 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphate + D-glucose.
COFACTOR: NAD and a divalent metal ion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: Optimum temperature is 40 degrees Celsius. Optimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDUCTION: By the five sucrose isomers and other alpha-glucosides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Hydrolyzes a wide variety of 6-phospho-alpha-D-glucosides including maltose-6/P, trehalose-6P and the 6'-phosphorylated derivatives of the five linkage-isomeric alpha-D-glucosyl-D-fructoses: trehalulose-6'P, turanose-6'P, maltulose-6'P, leucrose-6'P, and palatinose-6'P. However, sucrose-6P is not a substrate for malH, and this enzyme also fails to hydrolyze beta-O-linked phosphorylated disaccharides such as cellobiose-6'P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and strontium do not.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pH is 7.0-7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (but not by sucrose or glucose).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and nickel
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                                                                                                                                                                                                                                                                                                                                         P41253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD006892; GH_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immel S., Robrish S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ions enhance activity whereas magnesium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49712 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.7%;
62.5%;
                                                                                                                                      Actinobacteria (class);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAD (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
EE9D85B35FA8AF46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manganese; Iron; Cobalt; Nickel;
                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thompson J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2e+02;
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                                                                                                                             Actinobacteridae
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SEQUENCE FROM N.A.

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B
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                                                                       Query Match
Best Local
                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region of the lysA gene in Brevibacterium lactofermentum: of argS-lysA cluster expression by arginine.";
J. Bacteriol. 175:7356-7362(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marcel T., Archer J.A.C., Mengin-Lecreulx D., Sinskey A.J.; "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene."; mol. Microbiol. 4:1819-1830(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ATCC 13059 / AS019;
MEDLINE-91186817; PubMed-2
                                                                                                                 CONFLICT
SEQUENCE
                                                                                                                                             CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 13032 / DSM
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oguiza J.A., Malumbres M., Eriani G., Pisabarro A., Mateos L.M., Martin F., Martin J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94042911; PubMed=8226683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sharp P.M., Mitchell K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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                                                                                                                                                                                                                                                                                                Pfam; PF03485; N-Arg;
                                                                                                                                                                                                                                                                                                          InterPro; IPR001278; Arg_tRNA-synt_lc.
InterPro; IPR005148; N.
InterPro; IPR001412; tRNA-synt_I.
Pfam; PF00750; tRNA-synt_ld; 1.
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Corynebacterium glutamicum arginyl-tRNA synthetase.";
Mol. Microbiol. 8:200-200(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93268096; PubMed=8497194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A gene encoding arginyl-tRNA synthetase is located in the upstream
                                                                                                                                                                                                                                    Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                   TIGRFAMS; TIGR00456; argS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [DENTIFICATION
                                                                                                                                                                                          BINDING
383 VTLDDLVEA 391
                           1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP diphosphate + L-arginyl-tRNA(Arg).
SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                      $12227; $12227.
$42850; $42850.
                                                                                                                                                                                                                                                                                                                                                                                                 X54740; CAA38537.1; ALT_INIT.
Z21501; CAA79710.1; -.
AP005277; BAB98572.1; -.
                                                       6; Conserv
                                                                                                                                                                                                                                                                                 PR01038; TRNASYNTHARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yenomic sequence of Corynebacterium glutamicum ATCC 13032."; (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                 TIGR00456; args;
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513
540
550
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                                                         Conservative
                                                                                                                  AA;
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                                                                                                                                                                            378
377
355
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                                                                                                                 59723 MW;
                                                                       73.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20300 / NCIB 10025;
                                                                                                              RE; Protein biosynthesis; Ligase; ATP-binding.

"HIGH" REGION.

"KMSKS" REGION.

ATP (BY SIMILARITY).

G -> D (IN REF. 2).

I -> M (IN REF. 2).

V -> A (IN REF. 2).

V -> A (IN REF. 2).

Y -> R (IN REF. 2).

3 MW; 3AF724BDEE8DC4C1 CRC64;
                                                                       Score 28; 1
Pred. No. 2
                                                           Mismatches
                                                   DB 1;
2.5e+02;
2;
                                                                                     Length 550;
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ALD DESCRIPTION OF STREET 
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                                                                                                                                                                                                                                                                                                                                                                   DHB4_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence of a 39,411 bp DNA fragment covering the left end chromosome VII of Saccharomyces cerevisiae."; Yeast 12:1555-1562(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MNT2_YEAST P53059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-1,3-mannosyltransferase MNT2 (EC 2.4.1.-).
                                                                                                                                                   DHB4_MOUSE STANDARD; PRT; 735 AA P51660; P51660; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat Estradiol 17 beta-dehydrogenase 4 (EC 1.1.1 (17-beta-hydroxysteroid dehydrogenase 4). HSD17B4 OR EDH17B4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=97127827; PubMed=8972578;
Coissac E., Maillier E., Robineau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNT2 OR YGL257C OR NRD558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal-anchor; Golgi stack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X94357; CAA64130.1; -. EMBL; Z72779; CAA96977.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mannose residues of O-linked glycans-i-PATHWAY: Glycosylation.
                                                                                                                                Mus musculus (Mouse)
SEQUENCE FROM N.A
                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 VISDDLFES 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE MNN1/MNT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type II membrane protein. Golgi (Potential).
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187
558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AΑ;
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187
64852
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27
                                                                            Rodentia; Sciurognathi;
                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.7%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LUMENAL (POTENTIAL).
N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28; I
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
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                                                                                                                                                                              update)
1.1.1.62) (17-beta-HSD
4).
                                                                                                                                                                                                                                                                                                                                          735 AA
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                                                                                 Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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                                                                                 Murinae; Mus
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 102.7 kDa protein in PRP16-SRP40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _YEAST
                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                    and six new open reading frames."; Yeast 10:231-245(1994).
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=94262327; PubMed=8203164;
Garcia-Cantalejo J., Baladron V., Esteban P.F.,
                                                                                                                                                                                                            Remacha M.A., Revuelta J.L., Ballesta J.P.G., Jimenez A., del Rey F.; "The complete sequence of an 18,002 bp segment of Saccharomyces cerevisiae chromosome XI contains the HBS1, MRP-L20 and PRP16 genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steroid
ACT SITE
                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKR089C OR YKR409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YK69_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Normand T., Husen B., Leenders F., Pelczar H., Baert J.-L., Begue A., Flourens A.C., Adamski J., de Launoit Y.; "Molecular characterization of mouse 17 beta-hydroxysteroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity es 6; Conserv
  European
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TISSUE SPECIFICITY: PRESENT IN MANY TISSUES WITH HIGHEST CONCENTRATIONS IN LIVER AND KIDNEY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00106; adh_short; 1.
PF01575; MaoC_dehydratas; 1.
PF02036; SCP2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X89998; CAA62015.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
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Bioinformatics Institute.
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66.7%;
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E294D3B6A268D424 CRC64;
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RESULT 49
OL56_STRAT
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Best Local
                                        InterPro; IPR001031; Thioesteras
Pfam; PF00109; ketcacyl-synt; 2.
Pfam; PF00550; pp-binding; 2.
Pfam; PF00698; Acyl_transf; 2.
Pfam; PF00975; Thioesterase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OL56_STRAT
Q07017;
                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
              Pfam; PF02801; ketoacy1-synt_C; 2.
PROSITE; PS00012; PHOSPHOPANTETHEINE;
                                                                                                                                                         EMBL; L09654; AAA19695.1; -. HSSP; P25715; 1MLA.
                                                                                                                                                                                                                                                                                                                                                                        Swan D.G., Rodriguez A.M., Vilches C., Mendez C., Salas J.A.; "Characterisation of a Streptomyces antibioticus gene encoding I polyketide synthase which has an unusual coding sequence."; Mol. Gen. Genet. 242:358-362(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oleandomycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                 InterPro; IPR003880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinomycetales; Streptomycineae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                               LACTONE RING
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; $39130; $39130.
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PS00606; B_KETOACYL_SYNTHASE;
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IPR000794;
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                                                                                                              ; Ac_transferase.
; Ketoacyl-synt.
; Ppantne_attach.
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v; 1CFC03C4A6E64B9C CRC64;
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(See http://www.isb-sib.ch/announce/
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RESULT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NZJ4; 094835;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
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                                                                                                                                                                                                                                 Morgan K., Hudson T.J., Richter A.;
"ARSACS, a spastic ataxia common in northeastern Quebec, is caused by mutations in a new gene encoding an 11.5-kb ORF.";
                                                                                                                                                                                                                                                                     Engert J.C., Berube P., Mercier J., Dore C., Lepage P., Ge B.
Bouchard J.-P., Mathieu J., Melancon S.B., Schalling M., Land
                                                                                                                                                                                                                                                                                                MEDLINE=20120709; PubMed=10655055;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANT ALA-2619
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                           SACS OR KIAA0730
                                                                            Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which co for large proteins in vitro.";
DNA Res. 5:277-286(1998).
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                              Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
                                                                                                                                                                                                                   Nat. Genet. 24:120-125(2000).
                                                                                                                                                               MEDLINE=99087487; PubMed=9872452;
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                                        FUNCTION: MAY FUNCTION IN CHAPERONE-MEDIATED PROTEIN FOLDING TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE CENTRAL NERVOUS SYSTEM. ALSO FOUND IN SKELETAL MUSCLE AND AT LOW LEVELS IN
              DISEASE: DEFECTS IN SACS ARE THE CAUSE OF AUTOSOMAL RECESSIVE
                            PANCREAS.
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ACYL CARRIER (ACP) 1.
BETA-KETOACYL SYNTHASE 2.
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Pred. No. 1.8e+03;
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ACYL-ENZYME INTERMEDIATE.
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ACYL CARRIER (ACP) 2.
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W; 41AE78AAAEB61F86 CRC64;
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time
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SUMMARIES

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    Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W., Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen Phan H., Velasco N., Garnes J., Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andre Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S. Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A
Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Prediction of the coding sequences of unidentified human genes. VI The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97191544; PubMed=9039502;
Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O.,
Tanaka A., Kotani H., Miyajima N., Nomura N.;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 170-1165 FROM N.A.
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01-FEB-1997 (TrEMBLrel. 02,
01-MAR-2002 (TrEMBLrel. 20,
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    Trong S., Kobayashi A., Olsen A.O.,
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01-JAN-1998 (TrEMBLrel. 05, Createa)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update
Type I restriction modification enzyme, subunit M.
                                                                                                                                                                                                                                              Smith D. R., Doucette-Stamm I.A., DeLoughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothler B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
                                                                                                                                              Pfam; PF02506; Methylase M; 1.
Pfam; PF02384; N6_Mtase; 1.
PRINTS; PR00507; N12N6MTFRASE.
                                                                                                                                                                                     EMBL: AE000868; AAB85440.I; InterPro: IPR003665; Methylase_M. InterPro: IPR002296; N12N6_mtfrase. InterPro: IPR003356; N6_DNA_mtase. InterPro: IPR002052; N6_Mtase.
  465
                                                                                                           SEQUENCE
                                                                                                                               PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
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Pfam; PF00620; RhoGAP; 1.
SMART; SM00109; CI; 1.
SMART; SM000055; FCH; 1.
SMART; SM00324; RhoGAP; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
PROSITE; PS50041; DAG_PE_BIND_DOM_2; 1.
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InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000198; RhoGAP.
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VLEDDLIEA 473
                                                     Similarity 7; Conser
                                                                                                          proteome.
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1165 AA;
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                        71715 MW;
                                                                89.5%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.78;
88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127344 MW;
                                                               Pred. No.
                                                                         Score 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36;
                                                                                                    06D4F1076A5D5BAD CRC64;
                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92EF768CAFD458C9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   616 AA
                                                                         DB 17; Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 1165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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                                             0;
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                                            Gaps
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Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 19.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q94256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998
01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Geisel C., Bradshaw H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  031188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein SEQUENCE 174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases EMBL; U64849; AAC48055.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                     Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides)
  EMBL;
HSSP;
                                                                                                                                                                    MEDLINE=98389683; PubMed=9721307;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               Rhodobacter
                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129
                                                                  bisphosphate carboxylase/oxygenase-deficient mutant of Rhodobacter sphaeroides.";
                                                                                                                                                                                                STRAIN-HR;
                                                                                                                                               Qian
                                                                                                                                                                                                                                                                NCBI_TaxID=1063;
                                                                                                                   Expression of glnB and a glnB-like gene (glnK) in a ribulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VLXDDLLEA 9
     Bacteriol. 180:4644-4649(1998).

IBL; AF032116; AAC34721.1; -.

SSP; P05826; 2PII.
                                                                                                                                                                                                                                                                                                                                                                                        protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00118; SAPB; 1.
                                                                                                                                             Tabita F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000004; SapB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             (TremBLrel. 05, Created)
(TremBLrel. 05, Last seq
(TremBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19210 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.8%;
77.8%;
                                                                                                                                                                                                                                                                                                                      alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cosmid K04A8.";
EMBL/GenBank/DDBJ databases

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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PRODOM; PD001194; PII_g1NB; 1.
PROSITE; PS00638; PII_GLNB_CTER; 1.
PROSITE; PS00496; PII_GLNB_UMP; 1.
SEQUENCE 112 AA; 12142 MW; 85E0
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Interpro; IPR002332; PII_GlnB_UMP.
Pfam; PF00543; P-II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q50407
Q50407;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORF617 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valakunja N.; Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              madhusudan K., Nagaraja V.;
mycobacterium smegmatis DNA gyrase:
Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96118228; PubMed=8574396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiology 141:3029-3037(1995)
                                                                                                                                                                                                                                                                                                                            Hypothetical 91.7 kDa protein. SPAC1486.03C.
                                                                                                                                                                                                               schizosaccharomycetales;
                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UTK6;
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                                   STRAIN=972H-
                                                                                                                                                                                   Schizosaccharomyces
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McDougall R.C., Rajandream M.A.,
                                                                          SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 VLVDDLLE 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        616 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence up
(TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64938 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.2%;
87.5%;
                                                                                                                                                                                                                              Schizosaccharomycetaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85E0EEAAC9EB13C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279AC173E042BA8A CRC64;
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           Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       797 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 616;
               Seeger K., Harris D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium.
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RESULT 8
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
8,8a-deoxyoleandolide synthase 1.
MEDLINE=20363406; PubMed=10908114;
                                                                                  Actinomycetales; Streptomycineae; NCBI_TaxID=1890;
                                                                                                                                                              Streptomyces antibioticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C., Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E., Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V., "Oryza sativa chromosome 10 BAC OSJMBD0018B10 genomic sequence."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

InterPro; IPR00477; RyTse.
InterPro; IPR005162; Retrotrans_gag.
Ffam; PF03722; Retrotrans_gag; 1.
Prim; PF00708; rvt; 1.
Polivarorain. Dan Alicontal Pure.
                                                                                                                                                                                                   OLEAI
                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  Q9KIV4;
                                                                                                                                                                                                                                                                                                                                                                 Q9KIV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polyprotein; RNA-directed DNA polymerase. SEQUENCE 894 AA; 100800 MW; 821DF61EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLEL. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative plant disease resistance polyprotein OSJNBB0018B10.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 VLTDDILDA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9FWC7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9FWC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000467; G_patch. Pfam; PF01585; G-patch; 1. SMART; SM00443; G-patch; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AL133357; CAB62413.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTADDLLEA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             797 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.2%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 10;
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 3;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                PRT; 4150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6A54E06C35CD664A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              821DF61EE19B8B2E CRC64;
                                                                                                Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 894;
                                                                                             Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                     Query Match
              Matches
                         Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002106; AAtRNA_ligaseII.
InterPro; IPR001227; Ac_transferase.
InterPro; IPR0001227; Fabb.
InterPro; IPR000794; Ketoacyl-synt.
InterPro; IPR003880; Ppantine_attach.
InterPro; IPR003880; Ppantine_attach.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00698; Acyl_transf; 3.
                                                            PROSITE; PS00211; ABC_TRANSPORTER; 1. AIP-binding; Complete proteome. SEQUENCE 263 AA; 28452 MW; 42B303
                                                                                                        ProDom; PD000006; ABC_transportr; 1. SMART; SM00382; AAA; 1.
                                                                                                                                    Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL; AP002996; BAB48588.1;
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q98L75;
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence
01-UN-2002 (TrEMBLrel. 21, Last annotated)
ATP-binding protein of ABC transporter.
                                                                                                                                                                                                                    Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                 Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
                                                                                                                                                                                                                                                                                                                                       STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group:
                                                                                                                                                                                                                                                                                                                      MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                              Phyllobacteriaceae; Mesorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium loti (Mesorhizobium loti)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00550; pp-binding; 3.
TIGREAMS; TIGR00128; fabD; 3.
PROSITE; PS00339; AA TRNA_LIGASE_II_2; UNKNOWN_1.
PROSITE; PS50075; ACP_DOMAIN; 3.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 2.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q98L75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphopantetheine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02801; ketoacyl-synt_C; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shah S., Xue Q., Tang L., Carney J.R., Betlach M., McDaniel R., "Cloning, Characterization, and Heterologous Expression of a Polyketide Synthase and P-450 Oxidase Involved in the Biosynthesis of the Antibiotic Oleandomycin.", J. Antibiot. 53:502-508(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF220951; AAF82408.1; HSSP; P25715; 1MLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity nes 7; Conserv
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           Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00109; ketoacyl-synt; 3.
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                    81.6%;
75.0%;
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435261 MW; 9383296C4C16647D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.2%;
87.5%;
                 Score 31; DB 16;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                             42B3032FF840BE9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 AA.
                              DB 16; Length 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Glaser P., Frangeul L., Bloecker H., Brandt P., Chakraborty T.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
L Science 294:849-852(2001).
RESULT 11
Q8Y6F
ID Q8Y6F
AC 08Y6F
AC 08Y6F
AC 08Y6F
O1-MA
DT 01-MA
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DE Hypot
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; ALDYGU, LIN01843; -.
Listilist; LIN01843; -.
InterPro; IPR000515; BPD_transp.
Pfam; PF00528; BPD_transp; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
PROSITE: PS00402; GPD_TRANSP_INN_MEMBR; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q92AS6
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STRAIN=CLIP 11262 / SEROVAR 6A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1642;
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                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8Y6F5
   STRAIN-EGD-E / SEROVAR 1/2A;
MEDLINE=21537279; PubMed=11679669;
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.
                                                                                                                                                                                                                                                                                              Listeria monocytogenes
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein 1mo1732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8Y6F5;
                                                                                                                                                                                                                                                                                                                                                               LMO1732.
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                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                            NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                  jisteriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LXDDLLEA 9
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n; Complete proteome.
31102 MW; 3BDE99E47DB9B2FA CRC64;
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75.0%;
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Pred. No. 1.6e+02;
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Q9JVG6

RESULT 13

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Q9K0G7
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                                                                         Matches
                                                                                             Best
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR000515; BPD_transp.
pfam; pr00528; BPD_transp; 1.
pROSITE; pS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
pROSITE; pS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 276 AA; 31088 MW; 808E99E56DE9B2F8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294:849-852(2001)
                                                                                                                                                                                                                                                                                                                                    Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Nelson W.C., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09K067;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UTP--glucose-1-phosphate uridylyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9K0G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (serogroup B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MC58 / SEROGROUP B;
MEDLINE=20175755; PubMed=10710307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 ISDDLLEA 172
                                                                                                                                                                                                                                            EMBL; AE002419; AAF41061.1; TIGR; NMB0638; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                      SEQUENCE
                                                                                                                                                                       Transferase;
                                                                                                                                                                                         TIGRFAMs; TIGR01099; galU; 1
                                                                                                                                                                                                                            InterPro; IPR001825; NTP_transferase.
                                                                                                                                                                                                                                                                                     Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                           MC58."
                                                                                                                                                                                                                                                                                                                     Complete genome sequence of Neisseria meningitidis serogroup B strain
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130 ILADDLIDA 138
                                                                                             Local
                                    1 VLXDDLLEA 9
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                                                                                                                                                                                                             pF00483; NTP_transferase; 1.
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                                                                                           Similarity
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                                                                                                                                                      289 AA;
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                                                                                                                                                    Nucleotidyltransferase; Complete proteome
89 AA; 32030 MW; D8D76E2C692781FF CRC64;
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75.0%;
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55.6%;
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Pred. No. 1.
                                                                                 ω
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                                                                                                                  Score 31;
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                                                                                                 Pred. No. 1.7e+02;
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                                                                                 Mismatches
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1.6e+02;
                                                                                                                      DB 16; Length 289;
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RESULT 14
Q9ADK9
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SEQUENCE FROM N.A.
                                   the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                          Redenbach M., Kieser H.M., Denapaite D.,
Kinashi H., Hopwood D.A.;
                                                                      "A set of ordered cosmids and a detailed genetic and physical map for
                                                                                                                                                                                                                                                               Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                   MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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2SCK31.11C OR SCO4951.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 ILADDLIDA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A; MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris D.;
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55.6%;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 AA
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                                                                                                                               Eichner A., Cullum J.,
                                                                                                                                                                                                                                                                                        Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 289;
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Best Local Similarity
                                                                 Hypothetical protein SEQUENCE 497 AA;
                                                                                                                 Pfam; PF01485; IBR; 2.
                                                                                                                                                              Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF003137; AAB93644.1; -.
                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                       Murray J., Wohldmann P., Biewald T.; "The sequence of C. elegans cosmid C27A12."; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                   Waterston R.;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                  InterPro; IPR002867;
                                                                                                                                                                                                                                  "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigating biology. The C
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 57.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              001964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
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PRINTS; PR00069; ALDKETRDTASE
PRINTS; PR01577; KCNABCHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL451182; CAC18692.2; -.
EMBL; AL512667; CAD30937.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quaini M.A., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Metzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete SEQUENCE 345 AA; 37200 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000288; Aldo/ket_red; 1
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                                                        57341 MW;
        81.6%;
                                                                                                                                            Znf_C6HC
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17200 MW; 1702711E71DF697E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The C. elegans Sequencing Consortium.
Score 31;
                                                  157E61283A58656F CRC64;
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DB 5;
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Pred. No. 2.9e+02;

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Q93GY8
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QQKDQ7
AC QQ AC QQ
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Non-ribosomal peptide synthetase.
Streptomyces avermittis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q93GY8
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Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=21477403; PubMed=11572948;
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InterPro; IPR003880; ppantne_attach.
Pfam; PF00668; Condensation; 1.
Pfam; PF00550; pp-binding; 1.
PROSITE; PS50075; ACP_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolites.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
MEDLINE-20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., M.
Takami E., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus halodurans.
Bacitlus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9KDQ7;
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                                 55 VLDNDLLEA 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein BH1154.
        EMBL;
                                                                                                                                                   "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                          Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 VLLDDLAEA 262
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        AP001511;
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7; Conserv
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            BAB04873.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.6%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 2; Pred. No. 3.3e+02; Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Best Local
                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam; PF02518; HATPase_C; 1.
pfam; PF00512; signal; 1.
sMART; SM00304; HAMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003594;
InterPro; IPR003660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00387; HATPase_c; 1. SMART; SM00388; HiskA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003661; His_kinA.
InterPro; IPR004359; HIS_KIN_sig.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; P
Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FS(1)YB.
FS(1)YB OR FS OR EG:95B7.8 OR CG2706.
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076911;
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                                                                                                                                                                                                                                                                                                                                                                                      cell maintenance during Drosophi
Development 126:1833-1844(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99203434; PubMed=10101118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  581 ILIDDLFEA 589
                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF141673; AAD32687.1;
                                                                                                                                                                                                                                                                                                                                                                                                                   King F.J., Lin H.; "Somatic signaling mediated by fs(1)yb is essential for germline stem
                                                                                                    01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2001 (TrEMBLrel. 16, EG:9587.8 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                 Eukaryota; Metazoa; F
Pterygota; Neoptera;
                                                                          Drosophila melanogaster (Fruit fly)
                                                                                         FS(1)YB OR EG: 95B7.8 OR CG2706.
                                      Ephydroidea;
SEQUENCE FROM N.A.
                          NCBI_TaxID=7227;
                                                                                                                                                                                                                                          595 VLEDDALEA 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                           Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                  1 VLXDDLLEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                     Metazoa; Arthropoda; Tracheata; He
Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                           PRELIMINARY;
                                       Drosophilidae; Drosophila
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                                                                                                                                                                                                                                                                                                                                                     ; fs(1)Yb.
117465 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31;
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                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                        Last annotation
                                                                                                                                   Last sequence update)
                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                              Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                          Score 31;
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                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                         oogenesis.";
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                                                                                                                                                                              1042 AA
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                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                      Hexapoda; Insecta;
                                                                                                                        update)
                                                          Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 750;
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RABILLURIN, MyDAYALLA, AND HATTIS MANDEWS-PTANNKOCH C., BAIGWIN D., RA Balews R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brotterin P., Brottier P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Glerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Glerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Davies P., Derbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., RA Lasko P., Lei Y., Karpen G.H., K Z., Kennison J.A., Ketchum K.A., RA Lasko P., Lei Y., Karpen G.H., K Z., Kennison J.A., Ketchum K.A., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Nelson C.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Steen H., Sannders R.D.C., Scheeler F., Shen H., RA Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J., RA Yellas S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Zheng L., Zhong Y.H., Zhong W., Zhong W., Zhou X., Zhu X., Smith H.O.,
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Q9W4W2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Bash A., Bayendale J., Bayerster D., Bayerster B.D., Ballew R.M., Bash A., Bayendale J., Bayerster B.D., Bayerster B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FS(1)YB protein.
FS(1)YB OR FS OR EG:95B7.8 OR CG2706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9W4W2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Ferraz C., Vidal S., Brun C., Bucheton A., Demaille J.G.; "Sequencing the distal X chromosome of Drosophila melanogaster."; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0000928; fs(1)Yb
SEQUENCE 1042 AA; 117450 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL021728; CAA16820.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1998)
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1042;
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Q9н653
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                                                                                                                                                                                                                                                                                                RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
TISSUE-SMALL INTESTINE; Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashir Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T. Nakamura Y., Isogai T., Sugano S., "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AK026254; BAB15413.1; -.
                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel 16, Created)
01-MAR-2001 (TrEMBLrel 16, Last sequence update)
01-DEC-2001 (TrEMBLE-119, Last annotation update)
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                          CDNA: FLJ22601 fis, clone HSI04471.
                                                                                                           SEQUENCE FROM N.A
                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                         Q9н653;
                                                                                                                                                                                                                                                                      Q9н653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL032657; CAA21742.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
Y47H9C.12 protein.
Y47H9C.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9XWD3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harris B.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gibbs R.A., Myers E.W., Rubin G.M., "The genome sequence of Drosophila r Science 287.2185-2195(2000).
EMBL; AE003425; AAR45815.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0000928; fs(1)Yb. SEQUENCE 1042 AA; 117451 MW;
                                                                                                                                                                                                                                                                                                                                           61 VLGDDLME 68
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 AA;
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       8379 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              75.0%;
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                               8C0FDFD4E40EE817 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last
                                                                                                                                                                                                                                                                PRT;
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Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                162 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 72;
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                                                                       Tashiro H.,
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            050241;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
Transposase homolog.
                                                                                                                                                                                         O9ASD4;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
P0456F08.25 protein (B1142C05.7 protein).
P0456F08.25 OR B1142C05.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       050241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002048; EF-hand. SEQUENCE 162 AA; 19013 MW;
                                                                                                                            Oryza sativa (Rice), and Oryza sativa (Rice), and Oryza sativa (Japonica cultivar-group). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=4530, 39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae Rhizobiaceae; Rhizobium.
NCBI_TaxID-176299;
                                                                  STRAIN=CV. NIPPONBARE; Sasaki T., Matsumoto T., Yaman Oryza sativa nipponbare(GA3)
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF034769; AAC71784.1; Plasmid.
                                                                                                                                                                                                                                                                      Q9ASD4
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kalogeraki V.S., Winans S.C.;
"Wound-released chemical signals may elicit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pTiC58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobacterium tumefaciens (strain C58 / ATCC 33970).
         STRAIN-CV.
                        SEQUENCE FROM N.A.
                                              Submitted (NOV-2000) to
                                                          clone: P0456F08."
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobacterium tumefaciens strain containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99009000; PubMed=9791116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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nes 6; Conserv
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les 6; Conserv
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Matsumoto
            NIPPONBARE;
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75.0%;
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Τ.,
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Yamamoto K.;
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Pred. No.
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Pred. No.
                                                                   moto K.;
genomic DNA,
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2e+02;
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                                                                                                                                                             Embryophyta; Tracheophyta;
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                                                                      chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an octopine-type Ti
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RESULT
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Matches 5
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Best Local :
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                                                                                                                     "Direct Submission.";
Submitted (SEP-2001) to the El
EMBL; AC024809; AAF59543.1; -
InterPro; IPR003034; SAP.
Pfam; PF02037; SAP; 1.
SMART; SM00513; SAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 27.0 KDa protein.
Y536AR.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00450; RECOVERIN.

Prodom; PD000012; EF-hand; 1.

SMART; SM00054; EFF; 3.

PROSITE; PS00018; EFF HAND; UNKNOWN_1.

SEQUENCE 248 AA; 27764 MW; 473E5A6777612678 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP002901; BAB39425.1; -. EMBL; AP003410; BAB89107.1; -. HSSP; P36610; 1G8I.
                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Enkabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Oryza sativa (japonica cultivar-group) genomic DNA, clone:B1142C05.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002048;
InterPro; IPR001125;
                                                                                                 SEQUENCE
                                                                                                           Hypothetical protein.
                                                                                                                                                                                                                                                   Submitted (MAR-2000) to
                                                                                                                                                                                                                                                                "The
                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                           investigating biology. The C
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9N3G0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00036; efhand;
                                                                                                                                                                                                 Waterston R.;
                                                                                                                                                                                                              STRAIN=BRISTOL N2;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                   None;
                                                                                                                                                                                                                                                                            Latreille P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 LSDDLVEA 156
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66
                                               Local Similarity
nes 5; Conser
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                                                                                                                                                                                                                                                   sequence of C. elegans cosmid Y53G8AR."; itted (MAR-2000) to the EMBL/GenBank/DDBJ
ILNDDILDA 74
                      VLXDDLLEA 9
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                                                Conservative
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                                                                                                 AA;
                                                                                                 26960 MW;
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55.6%;
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75.0%;
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Pred. No. 2.3e+02;
1; Mismatches 1
                                                  ω,.
                                                                                                                                                                         EMBL/GenBank/DDBJ databases
                                              Score 30; DB 5;
Pred. No. 2.4e+02;
3; Mismatches 1
                                                                                                 F573AD88CD188DA1 CRC64;
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                                                                           253;
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Вb
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Q9R6D2
             Q8U5Z9
                           RESULT 27
                                                                                                                                    Query Match
Best Local :
                                                                                                                         Matches
                                                                                                                                                                                   "Genome structure of pTi-SAKURA (V): Complete nucleotide sequence plasmid pTi-SAKURA's vir region in Agrobacterium tumefaciens."; Nucleic Acids Symp. Ser. 39:265-266(1998).
EMBL; AB016260; BAA87753.1; -.
  Q8U5Z9
                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=MAFF301001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MART DULY ..., Ohta N., ULGJ. ..., HALTOTI Y., SUZUKİ K., Ohta N., ULGJ. ..., "Genome structure of pTi-SAKURA(I): Strategy Japanese cherry-Ti plasmid."; Japanese cherry-Ti plasmid."; Ser. 37:159-160(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=MAFF301001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98193120; PubMed-9524202; Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.; "Novel structural difference between nopaline- and octopine- type trbJ gene:construction of genetic and physical map and sequencing of trb/traI and rep gene clusters of a new Ti plasmid pTi-SAKURA."; Biochim. Biophys. Acta 1396:1-7(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                     Uraji M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-MAFF301001;
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete nucleotide sequence of a plant tumor-inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20184752; PubMed=10721727;
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                                                                                              2 LXDDLLEA 9
                                                                    LTDDVLEA
                                                                                                                      Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                       ., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.; structure of pTi-SAKURA (IV): Characteristics of tra region."; Acids Symp. Ser. 39:187-188(1998).
                                                                                                                                                                                                                                                                                                                                                                                     , Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K., structure of pTi-SAKURA (III): Characteristics of T-DNA.", Acids Symp. Ser. 39:185-186(1998).
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                                                                                                                      Conservative
 PRELIMINARY;
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75.0%;
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                                                                                                                   Score 30; DB Pred. No. 2.8e 1; Mismatches
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Last seq
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Last annotation updat
 PRT;
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302 AA
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Best Local :
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative NAD-binding protein.
SCO2824 OR SCBACT7F8.15.
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MEDILINE=21608550; PubMed=11743193;

WOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.,

Chura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Gordon I.

Kutyavin G., Rouse G., Saenphimmachak C., W. Z., Romero P., Gordon I.

Raymond C., Rouse G., Saenphimmachak C., W. Z., Romero P., Gordon I.

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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01-JUN-2002
01-JUN-2002
                                                                            STRAIN=A3(2);
O'Neil S., Ha
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                                                   Submitted (JUL-2001)
                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q93J73
SEQUENCE FROM N.A
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                         NCBI_TaxID=1902;
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75.0%;
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                                                   the EMBL/GenBank/DDBJ databases
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Dolan M.,
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Best Local :
                        STRAIN=A3(2);
Bentley S.D.,
Submitted (JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harris D.E., Quail M.A., Kieser H., Collins M., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K. Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 417:141-147(2002).
EMBL; AL596030; CAC44287.1; -.
InterPro; IPR002162; D_2hydac_dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A_3(2).";
                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosić eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                           Q9M1Q2;
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                                                                                                                                                                           Rieger M., Mueller-Auer S., Zipp M., Schaefer Lemcke K., Mayer K.F.X., Quetier F., Salanouba Submitted (FEB-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                    Serine/threonine protein kinase-like protein
                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
 ProDom;
                PRINTS;
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nes 6; Conserv
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NCE 327
PD000001; Euk_pkinase;
                 PR00109;
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AA; 34874 MW;
                 TYRKINASE
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٢
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46F9FEE02F62F28F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                             Schaefer M., Mewes Salanoubat M.;
                                                                                                                                                                                                                                                                                                                                                                                                          361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1e+02;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eichner A., Cullum J.,
                                                                                                              databases
OF PROTEII
                                                                                                                                                                                   databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 327;
                                                                                                                PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                              eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                physical map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.,
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09ESE8
                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00221; STYKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruepp
Mewes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding; Kinase; SEQUENCE 361 AA;
                                                                                                                               O9ESE8

O9ESE8;

O1-MAR-2001 (TrEMBLrel. 16,

O1-MAR-2001 (TrEMBLrel. 16,

O1-JUN-2002 (TrEMBLrel. 21,

O1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermoplasma acidophilum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein Ta0256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9HLH2;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9HLH2
                                                                                                               vi-mak-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation updat. Inhibitor of apoptosis protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 407:508-513(2000).
EMBL; AL445063; CAC11401.1; -.
Interpro; IPR002792; TRAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The genome sequence acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermoplasmataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea;
                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete SEQUENCE 401 AA; 45365 MW;
                         SEQUENCE FROM N.A. Holcik M., Lefebvr
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMs; TIGR00089; UPF0004;
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001861; UPF0004.
 "Cloning and Characterization Apoptosis Protein 1, 2, and 3
                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                            209
                                                                                                                                                                                                                   31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 ILADELIEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VLXDDLLEA
                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                     2 LXDDLLEA
                                                                                                                                                                                                                                                            ILDDLLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A., Gramı ...,
H.-W., Frishman D.,
                                                                                                                                                                                                                                                                                                                                                                                                           PF01938; TRAM; 1.
PF00919; UPF0004; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ū
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                6;
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; me sequence of the thermoacidophilic scavenger Thermoplasma
 Lefebvre C.A., Hicks K., Korneluk R.G.; nd Characterization of the Rat Homologs Protein 1, 2, and 3 Genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                            216
                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38994 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                             78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoplasmata; Thermoplasmatales;
                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                Score 30; DB 1/; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 10;
Pred. No. 3.4e+02;
                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73EFE078A1F498FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                      proteome.
30AB6D614E8D7ABA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401
               Homologs of the Inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                   update)
                                                                                  Muridae;
                                                                                                                                                                                                                                                                                                                                           Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                  Murinae;
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                                                                                  Rattus
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                                                                                                Matches
                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001841; Znf_ring.
Pfam; PF00653; BIR; 3.
Pfam; PP00619; CARD; 1.
Pfam; PF00097; Zf-C3HC4; 1.
SMART; SM00238; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00114; RING; 1.
                                                                                                                                                                                                                                                                                                                  Pfam; PF00619; CARD; 1.
Pfam; PF00097; zf-C3HC4; 1
SMART; SM00114; CARD; 1.
SMART; SM00114; CARD; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.; "Cloning of cDNA for rat inhibitor of apoptosis protein 2."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
--i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; AF190020; AAF04585.1; -.
HSSP; Q13490; 1QBH.
                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                            PROSITE; PS50143; BIR_RI PROSITE; PS50209; CARD;
                                                                                                                                                                                                                                                                 PROSITE; PS01282; BIR_REPEAT_1; 3. PROSITE; PS50143; BIR_REPEAT_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Inhibitor of apoptosis protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001315;
InterPro; IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9QZC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001370; BIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01282; BIR_REPEAT_1; PROSITE; PS50143; BIR_REPEAT_2; PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
  449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 ILDDLLEA 456
                                                                                                Local Similarity les 6; Conser
                                                                                                                                                                                                                    nc-finger
                                              2 LXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LXDDLLEA 9
ILDDLLEA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00653; BIR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF183431; AAG22971.1;
Q13490; 1QBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 6; Conserv
                                                                                                                                                                                                589 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589 AA;
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                             66777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66750 MW;
                                                                                                                       78.
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.9%;
75.0%;
                                                                                                                    .0%;
                                                                                                                                              .98;
                                                                                                                  Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB 11;
Pred. No. 5.7e+02;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                        E6812FFE3EA34142 CRC64;
                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B4F7089BD7CD285B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              589
                                                                                                                                       DB 11;
                                                                                                               .7e+02;
                                                                                                                                       Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 589;
                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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RESULT 34
Q9PD83
                  AX MEDLINE=20365717; PubMed=10910347;

AX MEDLINE=20365717; PubMed=10910347;

RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

RA Alvarenga R., Alves L.M.C., Braya J.E., Baia G.S., Baptista C.S.,

RA Alvarenga R., Alves L.M.C., Braya J.E., Baia G.S., Baptista C.S.,

RA Alvarenga R., Alves L.M.C., Bordin S., Bove J.M., Briones M.R.S.,

RA Colanto M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Carraro D.M., Carrer H.,

RA Colanto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,

RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

RA HO P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,

RA Krieger J.E., Kuramae B.E., Laigret F., Lambais M.R., Leite L.C.C.,

RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,

RA Marques M.V., Marrins E.A.L., Martins E.M.F., Matsukuma A.Y.,

RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
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Q9V1X8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2002 (TrEMBLrel. 20,
TonB-dependent receptor for
                                                                                                                                                                                                                                                                                                   STRAIN=9A5C
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     Xylella
                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                      Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9PD83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9PD83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        structure and evolution.";
submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AJ248283; CAB49220.1;
InterPro; IPR00365; Methylase_M.
InterPro; IPR002265; Methylase_M.
InterPro; IPR002256; No. INA. Mtase.
InterPro; IPR003355; No. Mtase.
InterPro; IPR00355; No. Mtase.
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                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02506; Methylase_M; 1.
Pfam; PF02384; N6_Mtase; 1.
PRINTS; PR00507; N12N6MTFRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Type____ restriction modification enzyme, subunit M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00092; N6_MTASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus abyssi.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ORSAY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAB2149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472 IVEDDLIEA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72679 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.9%;
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                                                                                                                                                                                                                                                                                                                                                                              gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation update) iron transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 1/;
Pred. No. 6.1e+02;
Pred. No. 6.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B87C455390DD8A03 CRC64;
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RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,

RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,

RA Quaggio R.B., Roberto P.G., Rodriques V., de Rosa A.J.M.,

RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,

RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,

RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,

RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,

RA de Salva A.C. R., Meidanis J., Setubal J.C.,

RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,

RA The genome sequence of the plant pathogen Xylella fastidiosa.";

RA LAROUST9; AAR84305.1;

REMBL; AROUST9; AAR84305.1;
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Best Local :
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                                                                                                                                                      Best
                                                                                                                                                                            Query Match
                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 683 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vankken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J., Salzberg S.L., White O., Fraser C.M.; "Oryza sativa chromosome 3 BAC OJIII_Bil genomic sequence."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative polyprotein, 5'-partial (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                         PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
Polyprotein; RNA-directed DNA polymerase.
NON_TER 1 1
                                                                                                                                                                                                                                         SEQUENCE
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90 VLTDELLDA
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                                                            1 VLXDDLLEA 9
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                                                                                                                                                   Similarity
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IPR001584; Rve.
IPR000477; RVTse.
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                                                                                                                                                                                                                                            799 AA;
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                                                                                                                         Conservative
      98
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75.0%;
                                                                                                                                                   78.9%; Score 30; DB 10; 66.7%; Pred. No. 7.9e+02;
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    Mismatches

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Pred. No. 6.7e+02;
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                                                                                                                                                                                                                                               223230AF54F2A818 CRC64;
                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 683;
                                                                                                                                                                                   Length 799;
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RESULT 36

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REGRESS REPRESENTATION OF THE PROPERTY OF THE 
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q89443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Immune protection conferred by the baculovirus-related glycoprotein of Thogoto virus (Orthomyxoviridae).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C., Rodriguez J.F., Vinuela E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BA71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gonzalez A., Calvo V., Almazan F., Almendral J.M., Ramirez J.C.,
La Vega I., Blasco R., Vinuela E.;
"Multigene families in African swine fever virus: family 360.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94233765; PubMed=8178480;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90219204; PubMed-2325202; Almendral J.M., Almazan F., Blasco R., Vinuela E.; "Multigene families in African swine fever virus: family 110.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90219205; PubMed=2325203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Camacho A., Vinuela E.;
"Protein p22 of African swine fever virus: an early structural protein that is incorporated into the membrane of infected cells.";
Virology 181:251-257(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BA71V;
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J. Gen. Virol. 74:1633-1638(1993).
                                                     Yanez R.J., Rodriguez J.M., Rodriguez J.F., Salas M.L., Vinuela I "African swine fever virus thymidylate kinase gene: sequence and transcriptional mapping.";
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94187118; PubMed=8139051;
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BA71V;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Almazan F., Murguia J.R., Rodriguez J.M., La Vega I., V Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                    Vinuela E.;
                                                                                                                                                                                                                                                                                                                                               Rodriguez
                                                                                                                                         MEDLINE=93346971; PubMed=8393914;
                                                                                                                                                                                                                                                                                   'Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virol. 64:2064-2072(1990).
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                                                                                                                                                                                                                                                              Virol.
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                                                                                                                                                                                                                                                           e families in African swine fever virus: 68:2746-2751(1994).
                                                                                                                                                                                                                                                                                                                                            J.M., Yanez R.J., Pan R., Rodriguez J.F., Salas M.L.,
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                                                                                                                       Salas M.L., Vinuela E.;
                                                                                                                                                                                                                                                                                               family 505.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vinuela E.;
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"Polyprotein processing in African swine fever virus: expression strategy for a DNA virus.";
                           MEDLINE=93327788; PubMed=8335009; Simon-Mateo C., Andres G., Vinuela
                                                             STRAIN-BA71V;
                                                                                                                                                                                                                         MEDLINE=90223993; PubMed=2327074;
Lopez-Otin C., Freije J.M., Parra F., Mendez E., Vinuela E.;
"Mapping and sequence of the gene coding for protein p72, th
capsid protein of African swine fever virus.";
Virology 175:477-484(1990).
                                                                           SEQUENCE FROM N.A.
                                                                                                        Gene 136:103-110(1993).
                                                                                                               Rodriguez J.M., Yanez R.J., Rodriguez J.F., Vinuela E., S
"The DNA polymerase-encoding gene of African swine fever
sequence and transcriptional analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93353606; PubMed=8102411; Rodriguez J.M., Yanez R.J., Almazan F., Vinuela E., Rodriguez J.F.; "African swine fever virus encodes a CD2 homolog responsible for the adhesion of erythrocytes to infected cells."; J. Virol. 67:5312-5320(1993).
                                                                                                                                                                  MEDLINE=94123986; PubMed=8293992;
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                                                                                                                                                                                                                                                                                                                                                                              "Two putative African swine fever virus helicases similar to yeast 'DEAH' pre-mRNA processing proteins and vaccinia virus ATPases DIIL
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94085774; PubMed=8262374;
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Yanez R.J., Boursnell M., Nogal M.L., Yuste L., Vinuela E.;
"African swine fever virus encodes two genes which share si
homology with the two largest subunits of DNA-dependent RNA
polymerases.":
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Munoz M., Freije J.M., Salas M.L., Vinuela E., Lopez-Otin
"Structure and expression in E. coli of the gene coding for
pl0 of African swine fever virus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90357780; PubMed=2389555; Blasco R., Lopez-Otin C., Munoz M
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STRAIN-BA71V;
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        a novel gene
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01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                              "Nucleotide sequence of
                                                                                                                                                                                                                                                         MEDLINE=94091056; PubMed=8266720;
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Pena L., Yanez R.J., Revilla Y., Vinuela E., So
"African swine fever virus guanylyltransferase
Virus 102-210
                                                                                                                                                                                                                                                                                                                  "A gene homologous to topoisomerase II in
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95159428;    PubMed=7856088;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Amino acid sequence and structural properties of protein p12, African swine fever virus attachment protein.";
                                                                                                                       584 LLADDLLE 591
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"Affican swine fever virus encodes a DNA ligase.";
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                                                                                                                                                                                                                   African swine fever virus.";
                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                        PubMed=1316688;
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75.0%;
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Last annotation update)
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l; Mismatches
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p17, a major
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RNA helicase

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Q8RG71
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EMBL; L00966; AAL31320.1;
InterPro; IPR001410; DEAD.
InterPro; IPR001464; DEAH_box.
InterPro; IPR001550; Helicase_C.
Pfam; PF00271; helicase_C: 1.
SMART; SM00490; HELICG: 1.
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                                                                                                                                                                                                                                                               STRAIN-CV. NIPPONBARE;
Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
Vanaken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
Salzberg S.L., White O., Fraser C.M.;
Salzberg S.L., White O., Fraser C.M.;
TOryza sativa chromosome 3 BAC OSUNBADOLIDEA genomic sequence.";
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O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                           Spermatophyta, Magnoliophyta, Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative polyprotein. osJNBA0010E04.6.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4530;
                                                                                                                                                                                                                                                  Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
Q8RG71;
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               Q8RG71
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75.0%;
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66.7%;
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Pred. No. 9.6e+02;
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RESULT 40
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QOKIZ9;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586.";
J. Bacteriol. 184:2005-2018(2002).
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MEDLINE=21886394; PubMed=11889109;
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                                                                                                                                                                            Tang L., Shah S., Chung L., Carney J., Katz L., Khosla C., Julien B.; "Cloning and heterologous expression of the epothilone gene cluster."; Science 287:640-642(2000).
                                                                                                                                                                                                                                                                                    cluster from Sorangium cellulosum.";
Gene 249:153-160(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                          Myxococcales;
                                                                                      HSSP; P14687; lAMU.
HSSP; P14687; lAMU.
InterPro; IPR001242; Condensatn.
InterPro; IPR001242; Condensatn.
InterPro; IPR001380; Ppantne_attach.
Pfam; PF00501; AMP-binding; l.
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                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20293058; PubMed=10831849;
                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SMP44;
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            PRINTS; PR00154; AMPBINDING.
PROSITE; PS50075; ACP_DOMAIN; 1.
PROSITE; PS00455; AMP_BINDING; 1
                                                                                                                                                                 EMBL; AF217189; AAF62881.1; -.
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Phosphopantetheine.
                                                                           Pfam; PF00668; Condensation;
                                                           Pfam; PF00550; pp-binding; 1.
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75.0%;
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    Mismatches

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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                            gene
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RESULT 42
Q8YWB9
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Q9P8H3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
ŚEÓUENCE FROM N.A.

MEDLINB=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, C
01-MAR-2002 (TrEMBLrel. 20, L
01-MAR-2002 (TrEMBLrel. 20, L
Hypothetical protein All1696.
                                                                                                                 Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae;
                                                                                                             NCBI_TaxID=103690;
                                                                                                                                                                                                                  98YWB9;
                                                                                                                                                                                                                             68MA8d
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
TIGREPANS; TIGR00614; recq; 1.
PROSITE; PS0690; DEAH_ATP_HELICASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9P8H3;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                            625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001410; DEAD.
InterPro; IPR002464; DEAH_box.
InterPro; IPR001650; Helicase_C.
InterPro; IPR004589; RecQ.
                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus nidulans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hofmann A.F., Harris S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomyc
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Emericella nidulans (Aspergillus nidulans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9P8H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Suppression of ATM kinase defects by mutation of a RecQ helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 LLDDMLEA 481
                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                1 VLXDDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                        VLDEDILEA 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               helicase MUSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tted (APR-2000) to the EMBL/GenBank/DDBJ databases. AF259396; AAF72650.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                           1534 AA;
                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1410 AA;
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                   78.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                   172538 MW; 705F553A7D34A684 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.9%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158078 MW; C5C3780DC293B3AA CRC64;
                                                                                                                                                                   Last annotation update)
                                                                                                                                                                                Last sequence update)
                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                   Score 30;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 2;
Pred. No. 1.4e+03;
1; Mismatches 1
                                                                                                                                                                                                                      PRT; 1999 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pezizomycotina; Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1534 AA
                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 1410;
                                                                                                                                                                                                                                                                                                                                                   6e+03;
                                                                                                                                                                                                                                                                                                                                                           Length 1534;
                                      K., Kimura T.,
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                 Gaps
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           Query Match
Best Local Similarity
Conserve
6; Conserve
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                                                                                                                                                                                                                                   InterPro; IPR001242; (InterPro; IPR000734; IInterPro; IPR003880; IInterPro; IPR001031; InterPro; IPR001031; I
                                                                                                          PRINTS: PRO0154: AMPBINDING.
PROSITE: PS50075; ACP_DOMAIN; 4.
PROSITE: PS00455; AMP_BINDING; 4.
PROSITE: PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
PROSITE: PS00100; LIPASE_SER; UNKNOWN_1.
                                                                                                                                                                           Pfam; PF00501; AMP-binding; 4. Pfam; PF00668; Condensation; 5. Pfam; PF00550; pp-binding; 4. Pfam; PF00975; Thioesterass; 1.
                                                                                               PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_2.
                                                                            SEQUENCE
                                                                                      Phosphopantetheine.
                                                                                                                                                                                                                                                                                                                                                             biosynthesis genes have homology with genes of the peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fiss E.H., Yu S., Jacobs W.R. Jr.; "Identification of genes involved in the sequestration of iron in mycobacteria: the ferric exochelin biosynthetic and uptake pathways.";
                                                                                                                                                                                                                                                                                       InterPro; IPR000873; AMP-bind.
InterPro; IPR000515; BPD_trans
                                                                                                                                                                                                                                                                                                                   HSSP; P14687; 1AMU
                                                                                                                                                                                                                                                                                                                              EMBL; AF027770;
                                                                                                                                                                                                                                                                                                                                                                          Yu S., Fiss E., Jacobs W.R. Jr.;
"Analysis of the exochelin locus in mycobacterium smegmatis:
                                                                                                                                                                                                                                                                                                                                                         tamily."
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98389687; PubMed=9721311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MC2155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       087314
087314;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95191405; PubMed=7885234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales; Corynebacterineae; Mycobacteriaceae; NCBI_TaxID=1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium smegmatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome SEQUENCE 1999 AA; 207906 MW; DC0751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
EMBL; AP003586; BAB78062.1; -.
1 VLXDDLLEA
                                                                                                                                                                                                                                                                                                                                            Bacteriol.
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                                                                           4976
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TremBLrel. 08, Created)
(TremBLrel. 08, Last sequence (TremBLrel. 20, Last annum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                        180:4676-4685(1998)
                                                                           AA;
                                                                                                                                                                                                                                                                                                                              AAC82550.1;
                                 78.9%;
66.7%;
                                                                                                                                                                                                                                                                      BPD_transp.
Condensatn.
                                                                        535912 MW;
                                                                                                                                                                                                                               Ppantne_attach.
Thioesterase.
                                                                                                                                                                                                                                                              Lipase.
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75.08;
                                            Score 30;
                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30;
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                    Mismatches
                                                                     39474A924441E03D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinobacteridae;
                                              DB 2;
                                 .3e+03
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                                            Length 4976;
                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                              synthetase
                  0;
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               Gaps
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Best Local (
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updata
Hypothetical protein NMA0574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Whitehead S., Spratt B.G., Barrell B.G.;
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STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;

STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;

MEDLINE-20222556; PubMed-10761919;

MEDLINE-2022556; PubMed-10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9JW27;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9JW27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         meningitidis 22491
                                                                                                                                                                                                                                                                                                                                              Lyons P.A., Armitage N., Argentina F., Denny P., Hill N.J., Lord C.J., Wilusz M.B., Peterson L.B., Wicker L.S., Todd J.A.; "Congenic mapping of the type 1 diabetes locus, idd3, to a 780-kb region of mouse chromosome 3: identification of a candidate segment of ancestral DNA by haplotype mapping."; Genome Res. 10:446-453(2000).

EMBL, AF19956; AAF32273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Testis nuclear RNA-binding IL2 OR TENR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome. SEQUENCE 78 AA; 8884 MW; A25602ACC1025941 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 404:502-506(2000).
EMBL; AL162753; CAB83865.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis (serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9JLB6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9JLB6
                                                                                                 Pfam; PF02137; A_deamin; 1. PROSITE; PS50141; A_DEAMIN_EDITASE; 1.
                                                                                                                                                                                                                                                             MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20243845; PubMed=10779485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LXDDLLE
                                                                                                                                                                                                       MGI:103258; Tenr.
MGI:96548; Il2.
rPro; IPR002466; A_deamin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria;
     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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     AA;
     9018 MW;
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85.7%;
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Pred. No. 1.
     OFE2FB5A803C0EB9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; J
Sciurognathi; Muridae;
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1.1e+02;
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RESULT 46
Q8UEB3
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Best Local Similarity
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                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L. Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin G., Rouse G., Saenphimmachak C., W. Z., Romero P., Gordo Ramm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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O1-JUN-2002 (TrEMBLrel. 21, C
O1-JUN-2002 (TrEMBLrel. 21, L
O1-JUN-2002 (TrEMBLrel. 21, L
Hypothetical protein Atul847.
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053107;
053107;
01-JUN-1998
01-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21608550; PubMed=11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C58."
        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Truncated Vaa surface lipoprotein adhesin (Fragment).
                                                                                                                                                                                                                                                                                       EMBL; AE009139; AAL42843.1; EMBL; AE008104; AAK87614.1;
                                                                                                                                                                                                                                                                                                                 "Genome sequence of the plant Agrobacterium tumefaciens C58 Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nester E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=176299;
                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 DDLLEA
                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 DDLLEA 9
                                                                                                                                                 69 LSDDLLE
                                                                                                                                                                             2 LXDDLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome of the natural genetic engineer Agrobacterium tumeraciens
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                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                             101 AA;
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                                                                                                                                                                                                        Conservative
                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                           protein; Complete
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                                                                                                                                                                                                                                                              11705 MW;
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                                                                                                                                                                                                                    76.3%;
85.7%;
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                                                                                                                                                                                                                                                                                                                               lant pathogen and biotechnology agent C58.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                        0;
                                                                                                                                                                                                        Pred. No. 1.50
0; Mismatches
                                                                                                                                                                                                                                 Score 29;
                                                                                 PRT;
                                                                                                                                                                                                                                                               E033AAA2AAEDA25D CRC64;
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                                                                                 103
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                                                                                                                                                                                                                                    DB 16;
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Q8ZR29
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Q9X834
                              RESULT 49
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Best Local :
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Best Local !
  Q8ZR29
                                                                                                                                                                                                                                                                          Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Rajendream M.A., Rutherford K., Rutter S., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                    Hypothetical protein SEQUENCE 119 AA;
                                                                                                                                                                                                         "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).", Old 11:41-147(2002).
Nature 417:141-147(2002).
EMBL, AL049727; CAB41560.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical protein SCO6067.
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2) / M145;
                                                                                                                                                                                                                                                                       Hopwood D.A.;
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Birkelund S.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The Mycoplasma hominis vaa/p50 genes structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01540; Lipoprotein_7; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma hominis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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                                                                        80 ILLSDLLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 LLVDDLLE
                                                                                                 1 VLXDDLLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VLXDDLLE 8
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                                                                                                                             Similarity 6; Conser
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  PRELIMINARY;
                                                                                                                             Conservative
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3.B., Christiansen G.;
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12250 MW;
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66.7%;
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75.0%;
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                                                                                                                     Pred. No. 1.76
1; Mismatches

    Mismatches

                                                                                                                                                      Score 29;
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Pred. No. 1.5e+02;
 PRT;
                                                                                                                                                                                AA5DBAD23E6BC065 CRC64;
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137 AA
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. 1.7e+02;
2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      display a mosaic gene
                                                                                                                                                    DB 16; Length 119;
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                                                                                                                                                                                                                                                                                           Taylor K.,
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Whitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).

EMBL; AL627267; CAD05075.1; -.
InterPro; IPR003736; DUF157.
Pfam; PF02584; DUF157; 1.
TIGRFAMs; TIGR00359; unchar_dom_1; 1.
Hypothetical protein; Complete proteome.
BQUENCE 137 AA; 14925 MW; 2C04E6D14B94F28B CRC64;
                                                                                                                                                                 MEDLINE-215/4947; PubMed-11677608;

Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0828K8 PRELIMINARY; PRT; 137 AA. 0828K8; PRELIMINARY; PRT; 137 AA. 01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 21, Last sequence up 01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8ZR29;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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Hypothetical protein; Complete proteome.
SEQUENCE 137 AA; 14939 MW; 2C04E6D152BC5018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413:852-856(2001).
EMBL; AE008723; AAL19550.1; -.
InterPro; IPR003736; DUF157.
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MEDLINE-21534948; PubMed-11677609;
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Search completed: December 27, 2002, 14:43:18

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Sequence 24, Appli Sequence 24, Appli Sequence 3, Appli Sequence 6, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 14, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 14, Appli Sequence 15, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 30, Appli Sequence 21, Appli Sequence 22, Appli Sequence 23, Appli Sequence 24, Appli Sequence 25, Appli Sequence 27, Appli Sequence 28, Appli Sequence 29, Appli Sequence 29, Appli Sequence 21, Appli Sequence 21, Appli Sequence 22, Appli Sequence 23, Appli Sequence 24, Appli Sequence 25, Appli Sequence 27, Appli Sequence 28, Appli Sequence 29, Appli Sequence 30, Appli Sequence 52, Appli Sequence 53, Appli	equence 33 equence 24 equence 24
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US-09-335-409-3
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US-09-428-517-2
Sequence 3, Application US/09335409
Patent No. 6121029
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
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CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER APPLICATION NUMBER: 60/120,254
EARLIER FILING DATE: 1999-02-16
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APPLICANT: BetLach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
APPLICANT: Tang, Li
APPLICANT: Tang, Li
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TYPE: PRT
ORGANISM: Artificial Sequence
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Pred. No. 4.1e+02;
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US-09-567-969-3
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; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-335-409-3
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Best Local
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
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PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
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CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT FILING DATE: 2000-05-10
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CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
CURRENT APPLICATION NUMBER: US/09/567,969
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Pred. No. 3.
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Operon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
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APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
FILE REFERENCE: 4-30582A
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APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
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Best Local Similarity
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                                                                                                                                                                                                                                                  Sequence 3, Application US/09568486 Patent No. 6355459 GENERAL INFORMATION:
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SEQ ID NO 3
LENGTH: 1410
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APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,480
CURRENT FILING DATE: 2000-05-10
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PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
                        APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,486
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
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APPLICANT: Ligon, James
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
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SOFTWARE: PatentIn Ver. 2.0
                 NUMBER OF SEQ ID NOS: 30
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Zirkle, Ross
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75.0%;
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Pred. No. 3.
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Pred. No.
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3.2e+02;
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTON: GENES FOR THE BIOSYNTHESIS OF
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,899
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARRE: Patentin Ver. 2.0
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; ORGANISM: Sorangium cellulosum US-09-567-899-3
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US-09-567-899-3
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LENGTH: 1410
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                                                                              SEQ ID NO 3
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APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
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TYPE: PRT
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75.0%;

    Mismatches

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Pred. No. 3.2e+02;
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Pred. No. 3.2e+02;
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            WESULT 10
US-08-674-168-29
Sequence 29, Application US/08674168
Patent No. 5804414
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                                                                                                                                                                                     Matches
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: Nucleic Acid Encoding Mutant Matrix
TITLE OF INVENTION: Proteins Useful for Attenuation or Enhancement of
TITLE OF INVENTION: Influenza A Virus, Vaccines and Methods of making and
                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: FOX. Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.048PC01
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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APPLICATION NUMBER: 08/471,100
FILING DATE: 6-JUNE-1995
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                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-SEPT-1994
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                                                                                                                                                                                                                                                                                                                                       251 amino acids
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                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                         not relevant
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29-SEPT-1995
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85.7%;
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75.0%;
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Pred. No.
                                                                                                                                                                                                 Score 28; DB 5; 1
Pred. No. 1.3e+02;
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RESULT 11
US-08-985-908-19
Sequence 19, Application US/08985908
Patent No. 6004773
GENERAL INFORMATION:
APPLICANT: MASAYUKI ARAKI, MASAK
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Best Local Similarity
Fights 6; Conserve
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; MOLECULE TYPE:
US-08-674-168-29
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APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-166541
FILING DATE: 30-JUN-1995
ATTORNEY/ACENT INFORMATION:
NAME: OBLON, NORMAN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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APPLICANT: SUGIMOTO, Masakazu
TITLE OF INVENTION: METHOD OF AMPLIFYING (
TITLE OF INVENTION: ARTIFICIAL TRANSPOSON
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 550 amino acids
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                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                         383 VTLDDLVEA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 413-2220
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 24, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08 FILING DATE: 01-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400 CITY: ARLINGTON
                                                                           COUNTRY:
                                                                                              CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                              STREET:
                                                                                                                               ADDRESSEE:
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MATSUI, Hiroshi
YOKOZEKI, Kenzo
                                                                                                              E: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                           USA
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HIRANO, Seiko
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 550;
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PC-DOS/MS-DOS

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-985-908-19
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Best Local Similarity
"~+~hes 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08852730
Patent No. 6090597
Patent No. 6090597
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,
APPLICANT: MASAKO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIHARA, AND TSUYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 8-142812
FILING DATE: 05-JUN-1996
ATTORNEY_AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                    TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE: FEO anino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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APPLICATION NUMBER: JP 8-325659
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DO SOFTWARE: Patentin Relo CURRENT APPLICATION DATA:
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LENGTH: 550 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
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PRIOR APPLICATION DATA:
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: VA
ZIP: 22026
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FILING DATE: 05-07-1997
                                            TOPOLOGY:
                                                                                                                      LENGTH:
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                                                                                                                      550 amino acids
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05-DEC-1997
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                                                                                                                                                                                                            RESULT 14
US-08-416-603-4
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Patent No. 5866780
GENERAL INFORMATION:
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Best Local Similarity
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Matches
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APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSH
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: JP 8-325658
FILING DATE: 05-DEC-1996
ATTORNEY, AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                TITLE OF INVENTION: Maize Chlorot.
TITLE OF INVENTION: Uses Therefor NUMBER OF SEQUENCES: 11
                                                                                    APPLICANT: Law, Marcus
APPLICANT: Hebara, Ledare
APPLICANT: Reddick, Bradford B.
TITLE OF INVENTION: Maize Chlorotic Dwarf Virus Genome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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les 6; Conserv
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66.78;
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    Mismatches

    Mismatches

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Pred. No. 3e+02;
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                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-4
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                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 4
                                                                            Matches
                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: McDaniel, Robert
APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029.00
CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER FILING DATE: 1999-02-16
EARLIER FILING DATE: 1999-02-16
EARLIER FILING DATE: 1999-02-16
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                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/106,100
EARLIER FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Betlach, Mary C. APPLICANT: Shah, Sanjay Kri
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 904-375-8100 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                   LENGTH: 3519
2421 LRDELLEA 2428
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NAME: LLOYd, Jeffrey
REGISTRATION UNMER: 35,589
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3457 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
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STATE:
                                      2 LXDDLLEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/416,603 FILING DATE:
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McDaniel, Robert
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GY: linear
                                                                          Conservative
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                                                                                          73.7%;
75.0%;
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                                                                                        Score 28; DB 4;
Pred. No. 2.4e+03;
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Pred. No. 2.3e+03;
                                                                        Mismatches
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RESULT 16

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Query Match
Best Local Similarity
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APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
APPLICANT: Tang, Li
APPLICANT: Tang, Li
APPLICANT: TANG, Li
APPLICANT: TOP INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08899330 Patent No. 6177275
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EARLIER FILING DATE: 1999-02-16
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
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CURRENT FILING DATE: 1999-10-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
            REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
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                                                                      APPLICATION NUMBER: 60/0:
FILING DATE: 24-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZÍ, LBUTA A
REGISTRATION NUMBER: 30,7
                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                    CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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APPLICANT:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
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TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                   USA
(212)8699741
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VENTION: PLANT NITROGEN REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAM, HON-MING
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75.0%;
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                                                                      30,742
                                                      5914-042-999

    Mismatches

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Pred. No. 2.6e+03
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            US-08-686-968C-192
Sequence 192, Application US/08686968C
Patent No. 6221361
GENERAL INFORMATION:
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                                                                         RESULT 19
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                                                                                                                                                                              Matches
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APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
APPLICANT: JUNKER, David E.
TITLE OF INVENTION: Recombi
APPLICANT: Cochran, Mark D.
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                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: LLC
STREET: New York
CITY: New York
                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400 TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                                                                                     184 ILSDDLL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/480,640A FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
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                                                                                                                                                                              Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                       linear
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71.4%;
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                                                                                                                                                                                                                                                                                                                                  192:
                                                                                                                                                                            Score 27; DB 3;
Pred. No. 2.6e+02;
1; Mismatches 1
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEO ID NOS: 231
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 192
LENGTH: 313
                                                                Matches
                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
                                                                                                                                                                                                                               TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO: 1
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ORGANISM: Swinepox virus
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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Local Similarity hes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1185 Average CITY: New York STATE: New York
                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: John P. White STREET: 1185 Avenue of the Americas
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                                1 VLXDDLL 7
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                                                                                                                                                                                             LENGTH:
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Junker, David E.
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                                                                Conservative
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71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant Swinepox Virus: 225
                                                                                71.18; 71.48;
                                                                                                                                                                                                                                 192:
                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 27; I
Pred. No. 2
                                                                                Score 27; DB 4;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
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                                                                                               Length 313;
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                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                  0;
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RESULT 21 US-08-375-992A-192

Sequence 192, Application US/08375992A

Patent No. 6328975

GENERAL INFORMATION:

APPLICANT: Cochran, Mark D. APPLICANT: Junker, David E.

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Query Match
Best Local Similarity
~*~hes 6; Conserv?
                                                                                  ; TYPE: PRT
; ORGANISM: Vigna
US-09-154-750A-89
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 22
US-09-154-750A-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-375-992A-192
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                     SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 89, Application US/09154750A Patent No. 6432640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/154,750A CURRENT FILING DATE: 1998-09-17 PRIOR APPLICATION NUMBER: 60/059,153 PRIOR FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                        APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
APPLICANT: Polyak, Kornelia
TITLE OF INVENTION: p53-Induced Apoptosis
FILE REFERENCE: 1107.75357
                                                                                                                                                                     NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/079817 PRIOR FILING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO:
                                                                                                                                    LENGTH: 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,992A
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 ILSDDLL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VLXDDLL 7
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                 Conservative
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                               71.1%;
66.7%;
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71.48;
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                               Score 27; DB 4;
Pred. No. 2.7e+02;
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Pred. No. 2.6e+02;
                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                 Length 324;
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               0;
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                 0,
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US-08-480-640A-114

Sequence 114, Application US/08480640A Patent No. 6033904 GENERAL INFORMATION:

APPLICANT:

Cochran, Mark Junker, David RESULT 25

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: Sequence US-09-562-737-7
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US-09-222-938A-31
; Sequence 31, Ap
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                                Qγ
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                                                                                                                                                                                                                                       SOFTWARE: Pate SEQ ID NO 7 LENGTH: 333
                                                                  Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09562737 Patent No. 6428967
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LENGTH: 324
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                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/222,938A CURRENT FILING DATE: 1998-12-30 NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Youngman, Philip
APPLICANT: Fritz, Chrisian
APPLICANT: Murphy, Christopher
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: ESSENTIAL E
FILE REFERENCE: 07334/060001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
267 MVDDLLES 274
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                                  2 LXDDLLEA 9
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                                                                                                                                                                                                                                                                             PatentIn Ver. 2.1
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                                                                    Conservative
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                                                                                      71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.18; 71.48;
                                                                                  Score 27; DB 4;
Pred. No. 2.8e+02;
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Pred. No. 2.7e+02;
Pred. No. 2.7e+02;
                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 324;
                                                                                                  Length 333;
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RESULT 26
US-08-295-802-114
US-08-295-802-114; Application US/08295802; Patent No. 6127163; Patent No. 6127163
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Best Local Similarity
"hehes 5; Conserv?
                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-480-640A-114
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 188
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Swinepox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: RENUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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MAP POSITION: ~23.2
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IMMEDIATE SOURCE:
CLONE: 515-85.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                  260 ILSDDLL 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/O: FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 389 amino
TYPE: amino acid
STRANDEDNESS: dou
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                                                                                                       CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Swir
STRAIN: Kasza
                                                                          COUNTRY: UZIP: 10112
                                                                                                                                        STREET:
                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNITS:
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                                                                                                                                                                                                                                                                                                                                                                                                1 VLXDDLL 7
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                                                                                                                                        E: John P. White
30 Rockefeller Plaza
                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             71.18;
71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 389;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 114, Application US/08488237A Patent No. 6251403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 114:
               TELEFAX: (212) 391-05
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDIVIDUAL ISOLATE:
IMMEDIATE SOURCE:
CLONE: 515-85.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: White, John P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS: LENGTH: 389 amino acids
                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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SEQUENCE CHARACTERISTICS:
                                                                 TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                  APPLICATION NUMBER: US/08/488,237A FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: John F. WHILL
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN: Kasza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                 TELEPHONE:
                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VLXDDLL 7
                                                                                                                                                                                                                                                                                         10036
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                                                                                                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : (212)977-9550
(212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Swinepox virus
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                                 391-0525
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71.48;
                                                   278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant Swinepox Virus
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                   114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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Pred. No. 3.3e+02;
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LENGTH:

389 amino acids

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US-08-375-992A-114
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Best Local Similarity 71.4%;
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                                                                                                                                                                                                        TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POSITION IN GENOME:
MAP POSITION: -2
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IMMEDIATE SOURCE:
CLONE: 515-85.1
                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cochran, Mark D. APPLICANT: Junker, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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MOLECULE TYPE:
STRAIN: Kasza
INDIVIDUAL ISOLATE:
IMMEDIATE SOURCE:
                                                              ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                   TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                          HYPOTHETICAL:
                                                                                                            MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: dou
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                         TYPE: amino acid
STRANDEDNESS: dou
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                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                  ORGANISM:
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                                                Swinepox virus
                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant Swinepox Virus 220
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Pred. No. 3.3e+02;
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US-08-375-992A-114
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                                                                                                        US-09-409-180A-1
                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kron, Micheal
APPLICANT: Hartlein, Micheal
APPLICANT: Michito, Hirikata
TITLE OF INVENTION: Human Asparaginyl-trna Synthetase DNA
FILE REFERENCE: Aparaginyl-trna Synthetase
CURRENT APPLICATION UNMER: US/09/167,299
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
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                                  Matches
                                                                  Query Match
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                                 Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/409,180A CURRENT FILING DATE: 1999-09-30 NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                              APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: White, David
APPLICANT: White, David
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 22196, A No. 6444802el Human Aminopeptidase
FILE REFERENCE: 5800-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATABASE ACCESSION NUMBER: X91009 DATABASE ENTRY DATE: 1996-08-21
                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 VLNDDLL 354
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nes 5; Conser
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2 LXDDLLE 8
                                  Conservative
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85.7%;
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71.48;
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                                  1; Mismatches
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Pred. No. 3.3e+02;
                                                   Score 27; DB 4;
Pred. No. 6.4e+02;
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RESULT 32
US-07-935-311A-4
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                                                                                                                                                                                                                       Sequence 4, Application US/07935311A Patent No. 5378809
                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Di Fiore, Pier Paolo
APPLICANT: Fazioli, Francesca
TITLE OF INVENTION: Substrate of the Epidermal Growth
TITLE OF INVENTION: Factor Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206)682-6031
TELEX: 3723336
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/646
FILING DATE: 28-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MAK1, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 9900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206,622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kawabata, Shunichiro
APPLICANT: Davie, Earl W.
TITLE OF INVENTION: MICROSOMAL ENDOPEPTIDASE
NUMBER OF SEQUENCES: 13
                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                            609 IADDLLE 615
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OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IN
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nes 5; Conserv
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COUNTRY: UZIP: 92660
                                STATE:
                                                CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive, 16th Floor
                                                                                                                                                                                                                                                                                                                                                              2 LXDDLLE 8
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USA
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6300 Columbia Center
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N-terminal
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71.48;
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Pred. No. 6.5e+02;
"'~matches 1; Indels
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Best Local :
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TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
                                                                                TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Di Fiore, Fig. 1907.
APPLICANT: Fazioli, Francesca
TITLE OF INVENTION: eps8, A Substrate for the Epidermal Growth Factor
TITLE OF INVENTION: Kinase, Antibodies Thereto, and Methods of Use Thereof
""""" OF SEOUENCES: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 821 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatib
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH035.001A
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 VMKDDVLE 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "1"
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TYPE: AMINO ACID
                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/368,079 FILING DATE: 03-JAN-1995
                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                          ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Newport Beach
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nes 5; Conserv
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FILING DATE: 19920825
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Pred. No. 7.6e+02;
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                                                                                                                                                                                                                               Sequence 41, Application US/08680326 Patent No. 5925733
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
                                                                       APPLICANT: BOSCH, MARNIX
APPLICANT: STRAND, KURT
APPLICANT: TODARO, GEORGE J.
APPLICANT: TODARO, GEORGE J.
TITLE OF INVENTION: DNA POLYMERASE OF GAMMA HERPES VIRUSES
TITLE OF INVENTION: ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL
TITLE OF INVENTION: FIBROMATOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                       APPLICANT:
APPLICANT:
                                   CORRESPONDENCE ADDRESS
                                                     NUMBER OF SEQUENCES:
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LENGTH: 821 amino acids
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: The Government of the United States, as represented by the APPLICANT: Secretary of Health and Human Services
TITLE OF INVENTION: Substrate of the Epidermal Growth Factor Kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              551 VMKDDVLE 558
 STREET:
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                   ADDRESSEE:
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755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                         ROSE, TIMOTHY M.
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Pred. No. 7.6e+02;
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; Patent No. 5756327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-452-083-2
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Best Local :
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                                               FILING DATE: 13-SEP-194
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,59
REFERENCE/DOCKET NUMBER: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 41:
TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240 TELEFAX: (617) 861-9540
                                                                                                                                          APPLICATION NUMBER: US/08/452,083
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/305,765
                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: RECOMBINANT MYCOBACTERIAL ISOLEUCYL-trna
TITLE OF INVENTION: SYNTHETASE GENES, TESTER STRAINS AND ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sassanfar, Mandana APPLICANT: Schimmel, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: SChiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 813-5600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 94304-1018
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                                                                    22,592
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Pred. No. 9.3e+02;
2; Mismatches 1;
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Best Local Similarity
"hehes 6; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-452-083-2
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SEQUENCE CHARACTERISTICS:
                                                                                                TELEFAX: (415) 576-0300 NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                       CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/724,643
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APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
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TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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MOLECULE TYPE:
                                                                                SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                  CLASSIFICATION:
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               TOPOLOGY:
                                STRANDEDNESS:
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Nakamura, Toru
Chapman, Karen B.
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Harley, Calvin
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peptide
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06-MAY-1997
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Pred. No. 9.9e+02;
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Matches 5; Conserv
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                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
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MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PARTON NUMBER: US 08/724,643
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APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                             FILING DATE: 14-AUG-PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
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ADDRESSEE: Townsend and Townsend and Crew LLP
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                     APPLICATION NUMBER:
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                  APPLICATION NUMBER:
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5. 6166178
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Chapman, Karen B.
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09-MAY-1997
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UMBER: WO PCT/US97/17618
01-OCT-1997
                                               UMBER: US 08/915,503
14-AUG-1997
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62.5%;
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Saccharomyces cerevisiae EST2p"
                                                                                                                      US 08/912,951
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

WO PCT/US97/17885

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Query Match
Best Local Similarity
Thehes 5; Conserve
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 259:
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ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Te
                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/854,050
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TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
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              CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                 FILING DATE: 06-MAY-1 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
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                                                                                                                                                      CLASSIFICATION: 536 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                           APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
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APPLICATION NUMBER:
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: United States of
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Two Embarcadero Center, 8th Floor
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62.5%;
                                                                                                                                    US 08/851,843
US 08/844,419
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RESULT 40
US-09-430-323-141
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
FORMATION FOR
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PRIOR APPLICATION DATA:
US 08/724,643
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LENGTH: 32 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "motif 4(B') peptide from OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
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                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                 ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cech, Thomas R.
                                                                                                                    PRIOR APPLICATION DATA:
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                                      APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997
                                                                             APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Embarcadero Center, 8th Floor
APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09430323
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Morin, Gregg B.
Harley, Calvin
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Nakamura, Toru
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62.5%;
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                                                                                                                                                                                                                       Version #1.30
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US-08-974-549A-46
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                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                      STREET: IWO CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                   PRIOR APPLICATION DATA:
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mes 5; Conserv
                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                  APPLICATION NUMBER: US/08/974,549A FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                      ZIP: 94111-3834
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APPLICATION NUMBER:
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TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6166178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997 APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /note= "motif 4(B') peptide from Saccharomyces cerevisiae EST2p"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 015389-002930US
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                                                                                                                                                                                                                                                                                                                                                                                             Two Embarcadero Center, Eighth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakamura, Toru
Chapman, Karen B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                              Townsend and Townsend and Crew LLP
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                               UMBER: US 08/844,419
18-APR-1997
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62.5%;
                                                                                                             US 08/724,643
US 08/846,017
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Pred. No.
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US-08-851-843A-124
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                              Sequence 124, Application US/08851843A Patent No. 6093809
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                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                            APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                              APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..35
OTHER INFORMATION: /note= "motif B' peptide from OTHER INFORMATION: Saccharomyces cerevisiae EST2p"
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ZIP:
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               COUNTRY:
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                                                                              ADDRESSEE:
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94111
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                                                San Francisco
                               California
                                                             )E: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
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                                                                                                                                                                              Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
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                                                                                                                                                                                                                             Lingner, Joachim
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             United States of America
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                                                                                                                                                                                                                                                  Thomas R
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Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 35;
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 244, Application US/08974549A Patent No. 6166178
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APPLICANT:
APPLICANT:
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 124:
                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                         APPLICANT:
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NAME: Apple, Randolph T
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/846,017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                           STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
STATE: California
             SOFTWARE:
                                                                                            COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 LVYDDLLE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VLXDDLLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 amino acids
                                                                                                                                                                                                                     Andrews, William H.
VENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                        Morin, Gregg B.
Harley, Calvin B.
                                                                                                                                                                                                                                                                                     Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                     Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                        Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
           PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                       Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                        Thomas R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.4%;
                                                                                                                                                                                                            727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 26; DB
Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 49;
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                                                                                                                                                                       Sequence 124, Application US/08854050 Patent No. 6261836
                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
                                                                                                                                                           GENERAL INFORMATION:
              APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
                                                APPLICANT:
APPLICANT:
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APPLICANT:
                                                                               APPLICANT:
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MOLECULE TYPE:
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NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,42
REFERENCE/DOCKET NUMBER:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 01-OCT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                           Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                          Lingner, Joachim
Nakamura, Toru
                                                                                                                                           Cech, Thomas R
                                                                                                                                                                                                                                                                                                                                     Conservative
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01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                               peptide
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62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244:
                                                                                                                                                                                                                                                                                                                                   2:
                                                                                                                                                                                                                                                                                                                                                Score 26; DB 4; Length 49; Pred. No. 53;
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Query Match
Best Local Similarity
Thes 5; Conserve
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US-09-430-323-124
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                                                                                                                                                                                                                       Sequence 124, Application US/09430323 Patent No. 6309867 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: linear
MOLECULE Type: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION UNAUER: US 08/844,419
FILING DATE: 18-APR-1997
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APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
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STREET: TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                           16 LVYDDLLE 23
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                                                 Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                      APPLICANT: Cech, Thomas R
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Nakamura, Toru
Chapman, Karen B.
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62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 49;
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Fights 5; Conserva
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US-08-851-843A-17
                                                                                                                                                                                                                                                                                                                                                   Patent No. 6093809
                                                                                                                                                                                                                                                                                                                                                                        Sequence 17,
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                             APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 LVYDDLLE 23
                                                                                         STREET: Two Embarcac
CITY: San Francisco
                                  ZIP: 94111
                                                      COUNTRY:
                                                                       STATE:
                                                                                                                              ADDRESSEE:
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APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 015389-002930US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 49 amino acids
                                                                       California
                                                                                                                                                                                                                                                                                                                                                                        Application US/08851843A
                                                                                                                                                                                                                     Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                          E: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                      United States of America
                                                                                                                                                                                                                                                                                              Lingner, Joachim
                                                                                                                                                                                                                                                                                                                    Cech, Thomas R
 Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB 4;
Pred. No. 53;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-300
                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
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                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
TYPE: amino acid
STRANDEDMESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION DATA:
PRIOR APPLICATION UNBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 25-APR--
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                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                         STREET: Two Embarcac
CITY: San Francisco
   FILING DATE:
                                                                                                MEDIUM TYPE:
                                                                                                                                                                  STATE:
                                                                                                                                                COUNTRY:
                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.4%;
Local Similarity 62.5%;
es 5; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/851,843A FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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                                                                                                                                    9411
                                                                                                                                                                 California
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                                                                                                                                                                                                                                                                                         Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                        E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                              United States of America
                                                                                                                                                                                                                                                           Andrews, William H.
VENTION: No. 6261836el Telomerase
                                                                                                                                                                                                                                                                                                                                                          Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                           Cech, Thomas R
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SYSTEM: PC-DOS/MS-DOS
UMBER: US/08/854,050
09-MAY-1997
                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
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25-APR-1997
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Pred. No. 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/09430323 Patent No. 6309867 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION NIMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 25-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                            ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                      Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cech, Thomas R
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                                                                                                                                                                                                               CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 amino acids
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Harley, Calvin
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Nakamura, Toru
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                                                                                                                                                                                               United States of America
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62.5%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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TYPE: amino acids
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-430-323-17
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US-09-153-599A-5
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Best Local Similarity 62...
S; Conservative
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Patent No. 6420177
GENERAL INFORMATION:
APPLICANT: Weber, J. Mark
APPLICANT: Luu, B. Minh
TITLE OF INVENTION: Method for Strain Improvement of
TITLE OF INVENTION: Erythromycin Producing Bacterium
NUMBER OF SEQUENCES: 13
                                                                                          ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V.

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: FER2

TELECOMMUNICATION INFORMATION:

TELECHIONE: 312-616-5400
                                  TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/153,599A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 LVYDDLLE 63
                                                                                                                                                                                                                    CLASSIFICATION: 435
                   LENGTH:
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
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amino acid
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FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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               241 amino acids
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PATENT NO. USUCCE

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5669
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US-09-134-001C-5669
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Search completed: December 27, 2002, 14:41:51 Job time: 27 secs
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NUMBER OF SEQ ID NOS: 5674
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LENGTH: 291
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Best Local Similarity
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino US-09-764-847-543
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US-09-764-847-543
                                         Matches
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                                                                                                                                                                                                                                                                                        Sequence 543, Application US/09764847 Patent No. US20020132767A1
                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
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OTHER INFORMATION:
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                                  Gaps
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7, Appli
46509, A
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10, Appl
34597, A
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13, Appl
32, Appl
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38358, A
1081, Ap
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40657, A
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RESULT

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Query Match
Best Local Similarity
Thes 6; Conserve
                                                                                           US-09-989-920-249
                                                                                                                RESULT 4
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                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapien US-09-989-920-200
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                                                    Sequence 249, Application US/09989920 Patent No. US20020172957A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-014-717-3
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
SEQ ID NO 200
LENGTH: 594
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: Publication No. US20020192778A1
: GENERAL INFORMATION:
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APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-yu
                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and
FILE REFERENCE: DEX-0291
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CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US/09/335,409
PRIOR ETLING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
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APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                  216 DDLLEA 221
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                                                                                                                                                                                                    4 DDLLEA 9
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                                                                                                                                                                                                                                     Conservative
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75.0%;
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                                                                                                                                                                                                                                                                Length 594;
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US-09-934-899-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09934899 Patent No. US20020102697A1
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LENGTH: 594
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Best Local Similarity 62.5%;
Matches 5; Conservative
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APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
NUMBER OF SEQ ID NOS: 284
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TITLE OF INVENTION: Genes encoding exopolysaccharide production
FILE REFERENCE: CL1633 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Sigun
APPLICANT: Wang, Tao
APPLICANT: Koffas, Mattheos
APPLICANT: Odom, J. Martin
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                                    APPLICANT: KOffas, Mattheos
APPLICANT: Odom, James M
APPLICANT: Odom, James M
APPLICANT: Schenzle, Andreas J
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: CL1596 US NA
CURRENT APPLICATION NUMBER: US/09/934,868
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
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SOFTWARE: Microsoft Office 97
                        NUMBER OF SEQ ID NOS: 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 DDLLEA 221
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RESULT 8 US-09-815-242-13677

Sequence 13677, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:

APPLICANT: Haselbeck, APPLICANT: Ohlsen, K

Robert

APPLICANT:

Ohlsen, Kari L. Zyskind, Judith W. Wall, Daniel

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; ORGANISM: Methylomonas 16a US-09-934-868-22
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; LENGTH: 293
                                                     Query Match
Best Local Similarity
Thes 6; Conserve
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; Patent No. US20020061569A1
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                                                                                                                                              ; TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13353
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13353
LENGTH: 296
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Best Local Similarity 62.5%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-12-22
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131 ILPDDLIE 138
266 VILQDLLEA 274
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                                 1 VLXDDLLEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen, Kari L.
Zyskind, Judith W.
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                                                                       Conservative
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                                                                                          73.7%;
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Pred. No.
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                                                                                          DB 10;
84;
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Trawick, John D.

Carr, Grant J

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Query Match
Best Local Similarity
Thes 6; Conserve
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 41433, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 6
PRIOR TILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                          PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-x-1
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR FILING DATE: 2000-08-03
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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                                                                                 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
APTITUG DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
                          FILING DATE:
                                     APPLICATION NUMBER: PCT/US01/00669
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Chen, Wensheng
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2000-02-04
NUMBER: US 60/207,456
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Patent No. US20020127584A1
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                                                                    CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
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                                    PRIOR APPLICATION NUMBER: 60/059266 PRIOR FILING DATE: 1997-09-18
                                                                                                                                                        FILE REFERENCE: P3430R1C1
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PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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TYPE: PI
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PRIOR APPLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                                                                                         Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                             Godowski, Paul
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                                                                                                                                                                                                                                                                       Smith, Victoria
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N: EXPRESSED IN HUNG, SIGNAL = 1.9

N: EXPRESSED IN LUNG, SIGNAL = 2.4

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.

N: EXPRESSED IN HELA, SIGNAL = 2.1

EXPRESSED IN HELA, SIGNAL = 3.
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EST_HUMAN
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HIT: AW963676.1,
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IN HEART, SIGNAL = 2.1
HIT: Q15034, EVALUE 7.00e-05
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IN LUNG, SIGNAL = 2.4
IN FETAL LIVER, SIGNAL = 1.6
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Pred. No.
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                          PRIOR FILING DATE: 2000-12-22
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PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/242,578
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                              APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/089514
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                  SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr, Grant J
                                                                                                                                                                                                                                                                                                                                                                                                                   Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto, Robert T.
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62.58;
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Pred. No.
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Query Match
Best Local Similarity
"~+~hes 5; Conserve
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                                                                                       US-09-952-013A-6
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US-09-815-915-11
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Matches
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LENGTH: 293
                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/952,013A CURRENT FILING DATE: 2001-09-14 PRIOR APPLICATION NUMBER: DECT/DE00/00767 PRIOR FILING DATE: 2000-03-08 PRIOR APPLICATION NUMBER: DE 199 11 992.9 PRIOR FILING DATE: 1999-03-17
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APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 3714, 16742, 23546, AND 13887 NOVEL
TITLE OF INVENTION: PROTEIN KINASE MOLECULES AND USES 1
FILE REFERENCE: 38155-20006.00
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                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                             APPLICANT: VINGRON, MARTIN
TITLE OF INVENTION: RNA POLYMERASE I TRANSCRIPTION FACTOR TIF-IA
FILE REFERENCE: 38485-0007
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CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,846
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 19
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                                                                                                ORGANISM: Arabidopsis thaliana
                                                                                                                        TYPE: PRT
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Pred. No. 2.9e+02;
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Pred. No. 1.9e+02;
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Pred. No. 1.3e+02;
              Mismatches
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LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-735-927-2
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US-09-735-927-2
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US-10-034-843-2
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APPLICANT: WEI, MING Hui et al.
APPLICANT: WEI, MING Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000834
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Matches
                 Sequence 2, Application US/10034843 Patent No. US20020111478A1 GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000834
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CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 60/231,570
PRIOR FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/231,570 PRIOR FILING DATE: 2000-09-11
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CURRENT FILING DATE: 2002-01-11
APPLICANT: Yu, Xuanchuan
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                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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83.3%;
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Pred. No.
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Pred. No. 3.2e+02;
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3.2e+02;
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; ORGANISM: homo sapiens US-10-034-843-2
В
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US-09-712-363-176
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                                                                                                                                                        ; ORGANISM: Mycobacterium tuberculosis US-09-712-363-176
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SOFTWARE: Fasts
SEQ ID NO 176
FENGTH: 1172
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                                                                            Matches
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Best Local
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TITLE OF INVENTION: No. US20020111478A1el Human Ion Channel Protein and Polynucleo
FILE REFERENCE: LEX-0291-USA
CURRENT APPLICATION NUMBER: US/10/034,843
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: US 60/258,334
PRIOR FILING DATE: 2000-12-27
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APPLICANT: Rotstein, Sergio
APPLICANT: Marcotte, Edwarn
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PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
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CURRENT FILING DATE: 2000-11-13
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PRIOR FILING DATE: 1999-05-14
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953 LPDELLEA 960
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                                     2 LXDDLLEA 9
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                                                                                              Similarity
                                                                                                                                                                                                                                                       FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rotstein, Sergio H. Marcotte, Edward M.
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                                                                            Conservative
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75.0%;
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Pred. No.
                                                                                            Score 27; DB 9;
Pred. No. 5.9e+02
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                                                                            Mismatches
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                                                                                                               Length 1172;
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; OTHER INFORMATION: /note= "motif 4(B') peptide from Saccharomyces cerevisiae EST2p" ; SEQUENCE DESCRIPTION: SEQ ID NO: 141: US-09-843-676-141
                                         RESULT 19
US-09-766-253-141
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Sequence 141, Application US/09766253 Publication No. US20020187471A1
                                                                                                                                                                                                                                                  Query Match
Best Local :
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                                                                                                                                  20 LYYDDLLE 27
                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                           1 VLXDDLLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
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Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide LOCATION: 1..32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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Chapman, Karen B.
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                                                                                                                                                                                                                                           68.4%;
62.5%;
                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                           Pred. No. 19;
                                                                                                                                                                                                                                                                Score 26; DB 9;
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US-09-823-266-19; Sequence 19, Application US/09823266; Patent No. US20020127688A1
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                                                                                                                                  GENERAL INFORMATION:
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                                                 APPLICANT:
                                                                                           APPLICANT: Burgess, APPLICANT: Arthur,
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 \begin{array}{lll} \text{APPLICANT:} & \text{Pietz, Bradley} \\ \text{TITLE OF INVENTION: Sigma binding region of RNA polymerase and uses thereof} \\ \end{array} 
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APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                   20 LVYDDLLE 27
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                             1 VLXDDLLE 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSEE: Townsend and Townsend and Crew LLP
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TITLE OF INVENTION: No. US20020187471A1el Telomerase
NUMBER OF SEQUENCES: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
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                                                 Bergendahl, Viet
                                                                       Anthony, Larry
                                                                                           Arthur, Terrance
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Morin, Gregg B.
Harley, Calvin
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                                                                                                                Richard
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62.5%;
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Pred. No. 19;
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Best Local (
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CURRENT APPLICATION NUMBER: US/09/823,266
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,116
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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TYPE: PRT
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PRIOR
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                                                           PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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PRIOR APPLICATION NUMBER: US 09/774,203 PRIOR FILING DATE: 2001-01-29
                                            PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: US 60/236,359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00666
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                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                               FILING DATE: 2001-01 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                               APPLICATION NUMBER: US 60/234,687
                                                                                                                      FILING DATE: 2001-01-30
                                                                                                                                       APPLICATION NUMBER: PCT/US01/00670
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د
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Chen, Wensheng
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RESULT 22
US-09-843-676-124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 124, Application Patent No. US20020164786A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 36279
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: MAP TO AC007114.7

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HELIOO, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94

OTHER INFORMATION: SWISSPROT HIT: P21529, EVALUE 4.70e-02

OTHER INFORMATION: EST_HUMAN HIT: AV705451.1, EVALUE 3.00e-18
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TYPE: PRT
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                      INFORMATION FOR SEQ ID NO: 124:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 IVDELLEA 27
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                                                           REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morin, Gregg B.
Harley, Calvin
Hadrey, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020164786Alel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
SEQUENCE
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/843,676 FILING DATE: 26-Apr-2001 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                             NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
                                                                                                                                                                                            APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
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                                        TELEFAX: (415)
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  CHARACTERISTICS
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Nakamura, Toru
Chapman, Karen B.
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62.5%;
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                                           576-0300
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Pred. No.
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28;
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Query Match
Best Local Similarity
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                                                                                                           ; SEQUENCE DESCRIPTION: SEQ ID NO: 124: US-09-766-253-124
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US-09-766-253-124
Sequence 124, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: APPLE, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERLISTICS:
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nes 5; Conser
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 124:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20020187471A1el Telomerase
NUMBER OF SEQUENCES: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                                                                                                   STRANDEDNESS: <Unknown>
                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/846,017 FILING DATE: 1997-04-25
                                                                                                                                                                                                                      LENGTH: 49 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                    Conservative
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Chapman, Karen B.
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62.5%;
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62.5%;
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                                                     Score 26; DB Pred. No. 31;
                                    Mismatches
                                                                      DB 9;
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                                                                      Length 49;
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                                    Indels
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RESULT 25
US-09-766-253-17
Sequence 17, Application US/09766253
; Publication No. US20020187471A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-843-676-17

Sequence 17, Application US/09843676;

Patent No. US20020164786A1

; GENERAL INFORMATION:
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                                                                                                                                56 LVYDDLLE
                                                                                                                                                                                                                   Local Similarity
mes 5; Conserv
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                                                                                                                                                                        1 VLXDDLLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: No. US20020164786Alel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T:
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997 APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/843,676 FILING DATE: 26-Apr-2001 CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 69 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                   Conservative
                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             San Francisco
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Nakamura, Toru
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                                                                                                                                                                                                                                       68.4%;
62.5%;
                                                                                                                                                                                                                                       Score 26; DE Pred. No. 44;
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                                                                                                                                                                                                                                                       Length 69;
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                                                                                                                      APPLICANT: Leach, I
APPLICANT: Mehrabs
APPLICANT: Conley
APPLICANT: Law, D
APPLICANT: Topper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                           Patent No. US20020082206A1
                APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
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PRIOR APPLICATION NUMBER: USSN 60/208,427
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                                                                                                                                                                                                                                                                                                                                                                                             56 LVYDDLLE 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Andrews, William H. TITLE OF INVENTION: No. US20020187471A1el Telomerase NUMBER OF SEQUENCES: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                           Mehraban, Fuad,
Conley, Pamela
Law, Debbie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/846,017 FILING DATE: 1997-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-Jan-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 69 amino acids
                                                                                                                                                                                                                                                                                Application US/09867550
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Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura, Toru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lingner, Joachim
                                                                                                                                                                                                                  Martin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
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Best Local Similarity
Thes 5; Conserve
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SEQ ID NO 599
LENGTH: 151
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NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
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Best Local :
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                                                                                                                                                                                                                Sequence 793, Application US/09925297 Patent No. US20020081659A1
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BRIOR APPLICATION NUMBER: PCT/US00/05918
BRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER FILING DATE: 1999-03-12
                CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR EILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
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CURRENT FILING DATE: 2001-08-10
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TYPE: PRT
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LOCATION: (1)
OTHER INFORMATION: wherein Xaa may be any one of Ala or Arg or Glu or Gln or Gly
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NUMBER OF SEQ ID NOS: 928
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LOCATION: (56)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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les 5; Conserv
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Pred. No.
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                                                                                                                                                                                                                                                                       Sequence 2, Application US/10013056 Patent No. US20020146728A1
                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 2
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                                                                                                                                                       APPLICANT: Ligensa, Tanja
APPLICANT: Schumacher, Ralf
APPLICANT: Weidner, Michael
TITLE OF INVENTION: IGF-1 Receptor Interacting Proteins
FILE REFERENCE: 09/453,195
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local :
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                                                                                                                       CURRENT APPLICATION NUMBER: US/10/013,056
CURRENT FILING DATE: 2001-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ligensa, Tanja
APPLICANT: Schumacher, Ralf
APPLICANT: Weidner, Michael
TITLE OF INVENTION: IGF-1 Receptor Interacting Proteins
FILE REFERENCE: 09/453,195
CURRENT APPLICATION NUMBER: US/09/917,974
CURRENT FILING DATE: 2001-07-30
                                                                                    PRIOR APPLICATION NUMBER: EPO 98122992.5 PRIOR FILING DATE: 1998-12-03
                                                                       NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/453,195
PRIOR FILING DATE: 1999-12-02
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TYPE: PRT
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TYPE: PRT
ORGANISM: Homo sapiens
                 LENGTH: 333
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62.5%;
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Pred. No. 2.4e+02;
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Pred. No. 1.3e+02;
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US-09-905-291A-255
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; Patent No. US20010016334A1
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                                                                                                                                                                                                                                                                                          APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                            Patent No. US20020160374A1
                                                                                                                                                                                                                                                                                                                                                                         Sequence 255, Application US/09905291A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/754,446
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/143,954
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 ILVDDVLTA 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
5; Conserv
                                                           Kljavin, Ivar J.
Mather, Jennie P.
                                                                           Hillan, Kenneth, J.
Kljavin, Ivar J.
                                                                                                                         Godowski, Paul J.
Grimaldi, Christopher
                                                                                                                                                                                                   Fong, Sherman
Gao, Wei-Qiang
Roy, Margaret Ann
Stewart, Timothy A.
                                             Pan, James
                                                                                                        Gurney, Austin L.
                                                                                                                                                                                                                                 Filvaroff, Ellen
                                Paoni, Nicholas F.
                                                                                                                                                       Goddard, A.
                                                                                                                                                                      Gerritsen, Mary E.
                                                                                                                                                                                       Gerber,
                                                                                                                                                                                                                                                                  Eaton, Dan L.
                                                                                                                                                                                                                                                                                Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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55.6%;
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83.3%;
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Pred. No. 3.3e+02;
"'Amatches 2;
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Pred. No.
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QΥ
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-291A-255
                                                                                                                                                                                                                                                        RESULT 33
US-09-902-853-255
                                                                                                                                                                                                                                                                                                                                  Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
NUMBER OF SEQ ID NO
SEQ ID NO 255
                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                       APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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APPLICANT:
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                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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APPLICATION NUMBER: PCT/US99/28565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US99/28564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US99/21090 FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US99/30999
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                                                                                                                                                                                 Genentech, Inc.
                                                                    Filvaroff, Ellen
                                                                                                         Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                             Ashkenazi, Avi
Botstein, David
               Gerber, Hanspeter
                                    Gao, Wei-Qiang
                                                   Fong,
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                                                     Sherman
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62.5%;
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Pred. No. 3.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 452;
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SEQ ID NO 255
                                                                             Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION UNMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
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CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US00/00219
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PRIOR APPLICATION NUMBER:
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PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
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                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US99/28214
                                                                                                                                                                                                              LENGTH: 452
352 IVDELLEA 359
                                      2 LXDDLLEA 9
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT, FILING DATE: 1999-12-20
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                                                                        Similarity
5; Conserv
                                                                                                                                                                      Homo Sapien
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Wood, William,
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Stewart, Timothy A.
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Mather, Jennie P.
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Grimaldi, Christopher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan, James
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                                                                             Conservative
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                                                                                         68.4%;
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                                                                                           Score 26;
Pred. No.
                                                                      Mismatches
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                                                                                                             DB 9;
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US-09-909-320-255; Sequence 255, Application US/09909320; Patent No. US20020132240A1

RESULT 34

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ORGANISM: Homo Sapien US-09-909-320-255
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Query Match
                                                                                   SEQ ID NO 255
LENGTH: 452
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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                                                                                                                                                                           PRIOR FILING DATE: 1999-12-20
                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT PRIOR FILING DATE: 1999-12-16
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                                                                                                                       NUMBER OF SEQ ID NOS: 423
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US99/30999
                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US99/30911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
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                                                                                                                                                           APPLICATION NUMBER: PCT/US00/00219
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Stewart, Timothy A.
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Hillan, Kenneth, J.
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Eaton, Dan L.
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68.4%;
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Score 26;
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RESULT 35
US-09-909-088B-255
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Matches 5; Conservative
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                                PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
                                                                                                   PRIOR APPLICATION NUMBER: PCT PRIOR FILING DATE: 1999-12-02
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PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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PRIOR APPLICATION NUMBER: PCT/US99/28313
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PRIOR APPLICATION NUMBER:
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PRIOR FILING DATE:
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                  APPLICATION NUMBER: PCT/US99/30911
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Ashkenazi, Avi
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Cao, Wei-Qiang
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Grimaldi, Christopher
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Hillan, Kenneth, J.
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TYPE: PRT,
; ORGANISM: Streptococcus pneumoniae
US-09-754-446-2
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Best Local Similarity
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TYPE: PRT
CRGANISM: Homo Sapien
US-09-909-088B-255
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CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/143,954
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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                        TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 255
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              APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                         Carr, Grant J.
Yamamoto, Robert T.
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Pred. No. 3.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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105.VLRDDIGEA 113

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Qγ
                                                                                                            ; ORGANISM: Pseudomonas aeruginosa US-09-815-242-5140
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                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-815-242-5140
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5140
LENGTH: 568
                                        Matches
                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT:
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Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA 011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith V
                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 457
                                      Local Similarity
nes 6; Conser
1 VLXDDLLEA 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto, Robert T.
                                      Conservative
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                                                    68.4<del>8</del>;
66.7<del>8</del>;
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55.6%;
                                                    Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 10;
Pred. No. 3.4e+02;
                                  Mismatches
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                                                    4.3e+02;
                                                                      DB 10;
                                                                      Length 568;
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US-10-071-751-30
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US-10-115-178-1
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Patent No. US20020142352A1
GENERAL INFORMATION:
                                                                                                                                                                                     Sequence 1, Application US/10115178 Patent No. US20020119135A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weber, Eric R.
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/171,156
FILING DATE: 1998-10-09
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hunter, Shirley Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                       Dickens, Martin
TITLE OF INVENTION: INHIBITORS OF THE JNK SIGNAL
TRANSDUCTION PATHWAY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                   APPLICANT: Davis, Roger J.
                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/071,751
FILING DATE: 07-Feb-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C4-PUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1560 BROADWAY, SUITE 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Xaa = any amino acid
LOCATION: 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 586 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 303/863-0223
CITY: Boston
                    STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80202
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44.4%;
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Pred. No. 4.5e+02;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 586;
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Query Match
Best Local Similarity
6; Conserva
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                                                                                                        US-09-767-870-8
                                                                                                                                        ; SEQ ID NO 8
; LENGTH: 709
; TYPE: PRT
                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/U
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 60/14
PRIOR FILING DATE: 1999-07-23
PRIOR APPLICATION NUMBER: 60/14
PRIOR FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: 60/16
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ruben e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 8, Application US/09767870
Patent No. US20020037549A1
                                   Matches
                                                Best Local Similarity
                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PT010P1
CURRENT APPLICATION NUMBER: US/09/767,870
CURRENT FILING DATE: 2001-01-24
                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ABC
                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                               PRIOR FILING DATE: 1 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           571 VKADDALEA 579
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
4 DDLLEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 07917/037001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/819,177 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 660 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben et al
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                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            ABC Transport Polynucleotides, Polypeptides, and Antibodies
                                                                                                                                                                                                                                                                                                                                                       2001-01-24
BER: PCT/US00/19736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.4%;
66.7%;
                                                    68.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26; DB 12;
Pred. No. 5.1e+02;
                                   Score 26; DB 10;
Pred. No. 5.5e+02;
1; Mismatches 0;
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                                                                        DB 10; Length 709;
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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US-09-770-689A-5
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                                                                                                                                                                                                                                                          RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-060-230-24
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GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED !
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                                                                                                                           Sequence 5, Application US/09770689A Patent No. US20020115171A1
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LENGTH: 736
TYPE: PRT
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Best Local :
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SEQ ID NO 24
LENGTH: 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HILTUNEN, Kalervo
TITLE OF INVENTION: A method to control cellular (3R)-hydroxyacyl-CoA
TITLE OF INVENTION: esters, precursor molecules for polyhydroxyalkanoate
TITLE OF INVENTION: synthesis in genetically modified organisms
FILE REFERENCE: 0365-0528p
CURRENT APPLICATION NUMBER: US/10/060,230
CURRENT FILING DATE: 2002-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Patent No. US20020173014A1
GENERAL INFORMATION:
APPLICANT: HILTUNEN, Kalervo
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CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 1991667
PRIOR FILING DATE: 1999-08-03
NUMBER OF SED ID NOS: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                             204 VMPEDLVEA 212
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5; Conserv
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55.6%;
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55.68;
HUMAN RAS-LIKE PROTEINS,
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Pred. No. 5.7e+02;
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US-09-770-689A-2
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
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CURRENT FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
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Patent No. US20020115171A1
GEMERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
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Best Local Similarity
Matches 5; Conserv
CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 780
TYPE: PRT
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                                                                                                              TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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TITLE OF INVENTION: PRO-
FILE REFERENCE: CL001079
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ORGANISM: HUMAN
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nes 5; Conserv
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Yamamoto, Robert T.
Xu, H. Howard
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62.5%;
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Pred. No. 6.3e+02;
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Pred. No. 6.1e+02;
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APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: 05/09/887,586A
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR APPLICATION NUMBER: 60/130,628
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Patent No. US20020164736A1
GENERAL INFORMATION:
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11216
LENGTH: 829
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Matches 5; Conser
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.1
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CURRENT FILING DATE: 2002-01-07
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APPLICANT: Schepmann, Hala G
TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
FILE REFERENCE: P02081US1
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                                                                                                                                                                                    APPLICANT: Chappell, Joseph APPLICANT: No. US20020094556All, Joseph P.
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TYPE: PRT
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55.6%;
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Pred. No.
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Pred. No. 6.8e+02;
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CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
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LENGTH: 868
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 56, Application US/09903012 Patent No. US20020094557A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                           Sequence 2, Application US/09816860A Patent No. US20020081651A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 26649, A No. US20020081651A1el Human GTPase Activating Molecul
TITLE OF INVENTION: Uses Therefor
FILE REFERENCE: MNI-133
CURRENT APPLICATION NUMBER: US/09/816,860A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/191,859
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 3
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PRIOR FILING DATE: 1999-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SYNTHASES FILE REFERENCE: 07678-025001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 58
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Pred. No. 6.8e+02;
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SOFTWARE: PatentIn Ver. 2.0

